

STIC-Biotech/ChemLib

89049

From: Bunner, Bridget
Sent: Friday, March 14, 2003 8:01 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/686,020:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647
CM1-10D12
(703) 305-7148
mailbox 10B19

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

RECEIVED
MAR 14 2003
STIC

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

24

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 03-17-03
Searcher: Beverly e 49914
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ _____ Other CGN

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:07:45 ; Search time 11 Seconds
(without alignments)
1319.701 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEQNGSTYYEENEMNG.....VEEPDPSGPTSTFSI 350

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 1819 | 100.0 | 350 | 1 CCR6_HUMAN | Q9NPB9 homo sapien |
| 2 | 1620 | 89.1 | 350 | 1 CCR6_BOVIN | P53350 bos taurus |
| 3 | 659 | 36.2 | 378 | 1 CCR7_HUMAN | P32248 homo sapien |
| 4 | 650 | 35.7 | 378 | 1 CCR7_MOUSE | P47774 mus musculu |
| 5 | 639 | 35.1 | 369 | 1 CCR9_MOUSE | Q9WU77 mus musculu |
| 6 | 637 | 35.0 | 357 | 1 CCR9_HUMAN | P51686 homo sapien |
| 7 | 605 | 33.3 | 367 | 1 CCR6_MOUSE | O54689 mus musculu |
| 8 | 583 | 32.1 | 374 | 1 CCR6_HUMAN | P51684 homo sapien |
| 9 | 581 | 31.9 | 342 | 1 CCR6_CERAE | O18983 cercopithe |
| 10 | 571 | 31.4 | 343 | 1 CCR6_MACMU | Q9X145 macaca mula |
| 11 | 569 | 31.3 | 342 | 1 CCR6_MACNE | O19024 macaca neme |
| 12 | 560 | 30.8 | 342 | 1 CCR6_HUMAN | O00574 homo sapien |
| 13 | 537.5 | 29.5 | 360 | 1 CCR4_HUMAN | P51679 homo sapien |
| 14 | 534.5 | 29.4 | 360 | 1 IL8B_HUMAN | P25025 homo sapien |
| 15 | 529.5 | 29.1 | 353 | 1 IL8B_HUMAN | P28807 pan troglod |
| 16 | 527 | 29.0 | 384 | 1 CCR6_HUMAN | O00590 homo sapien |
| 17 | 525 | 28.9 | 362 | 1 CCR4_HUMAN | P54111 ratius norv |
| 18 | 524 | 28.8 | 354 | 1 CCR4_HUMAN | Q28422 gorilla gor |
| 19 | 522.5 | 28.7 | 353 | 1 IL8B_GORGO | P49238 homo sapien |
| 20 | 522.5 | 28.7 | 355 | 1 CCR4_HUMAN | P51680 mus musculu |
| 21 | 521.5 | 28.7 | 353 | 1 IL8B_MOUSE | Q28519 macaca mula |
| 22 | 520.5 | 28.6 | 352 | 1 CCR4_MOUSE | O91121 mus musculu |
| 23 | 512 | 28.1 | 356 | 1 IL8B_MOUSE | O97571 canis fami |
| 24 | 512 | 28.1 | 354 | 1 CCR4_MOUSE | Q9Z049 mus musculu |
| 25 | 511 | 28.1 | 358 | 1 IL8B_MOUSE | P53344 mus musculu |
| 26 | 511 | 28.1 | 358 | 1 IL8B_MOUSE | P53344 mus musculu |
| 27 | 504 | 27.7 | 355 | 1 CCR2_MACMU | O18793 macaca mula |
| 28 | 501.5 | 27.6 | 355 | 1 IL8A_RABIT | P21109 oryctolagus |
| 29 | 500.5 | 27.5 | 358 | 1 CCR3_CAVO | O92213 cavia porce |
| 30 | 500.5 | 27.5 | 352 | 1 CCR4_HUMAN | P30991 homo sapien |
| 31 | 499.5 | 27.5 | 353 | 1 CCR4_BOVIN | P25930 bos taurus |
| 32 | 499.5 | 27.5 | 360 | 1 IL8B_BOVIN | Q28003 bos taurus |
| 33 | 498.5 | 27.4 | 352 | 1 CCR4_PAPAN | P56491 papio anubi |

| | | | | | |
|----|-------|------|-----|--------------|--------------------|
| 34 | 498.5 | 27.4 | 352 | 1 CCR5_CERTO | O62743 cercocebus |
| 35 | 498.5 | 27.4 | 353 | 1 CCR4_FELCA | P56498 felis silve |
| 36 | 497.5 | 27.4 | 350 | 1 IL8A_GORGO | P55919 gorilla gor |
| 37 | 495.5 | 27.2 | 352 | 1 CCR5_CERAE | P56493 cercopithe |
| 38 | 494.5 | 27.2 | 352 | 1 CCR4_CERTO | O62747 cercocebus |
| 39 | 493.5 | 27.1 | 352 | 1 CCR4_MACFA | Q28474 macaca fasc |
| 40 | 493.5 | 27.1 | 352 | 1 CCR4_MACMU | P79394 macaca mula |
| 41 | 492.5 | 27.1 | 359 | 1 CCR3_RAT | O54814 ratius norv |
| 42 | 492.5 | 27.1 | 359 | 1 IL8B_RAT | P35407 ratius norv |
| 43 | 491.5 | 27.0 | 352 | 1 CCR5_PAPHA | P56441 papio hamed |
| 44 | 491.5 | 27.0 | 352 | 1 CCR5_PYGAT | O97880 pygathrix b |
| 45 | 490.5 | 27.0 | 352 | 1 CCR5_MACMU | P79436 macaca mula |

ALIGNMENTS

RESULT 1
ID CCR6_HUMAN STANDARD; PRT; 350 AA.
AC Q9NPB9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 11 (C-C CCR-11) (CCR-11)
DE (Chemokine receptor-like 1) (CCR1L) (CCX CCR).
GN CCR1 OR CCR2 OR VSHK1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20200450; PubMed=10734104;
RA Schweickart V.U., Epp A., Raport C.J., Gray P.W.;
RT "CCR1L is a functional receptor for the monocyte chemoattractant
protein family of chemokines.";
RT J. Biol. Chem. 275:9550-9556(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171478; PubMed=10706668;
RA Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,
Schall T.J.;
RT "Cutting edge: Identification of a novel chemokine receptor that binds
dendritic cell- and T cell-active chemokines including ELC, SLC, and
TECK.";
RT J. Immunol. 164:2851-2856(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231748; PubMed=10767544;
RA Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;
RT "Cloning of CCR1L, an orphan seven transmembrane receptor related to
chemokine receptors, expressed abundantly in heart.";
RL Gene 246:229-238(2000).
CC - FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4,
SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, LOWER
EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL
TISSUES.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL: AF193507; AAF61299.1; -
CC EMBL: AF233281; AAF44751.1; -
CC EMBL: AF110640; AAF59827.1; -
DR

DR Genev; HGNC:1611; CCRL1.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PS00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 42
 FT TRANSSEM 43 63
 FT TRANSSEM 64 87
 FT TRANSSEM 88 108
 FT TRANSSEM 109 113
 FT TRANSSEM 114 134
 FT TRANSSEM 135 154
 FT TRANSSEM 155 175
 FT TRANSSEM 176 201
 FT TRANSSEM 202 222
 FT TRANSSEM 223 240
 FT TRANSSEM 241 261
 FT TRANSSEM 262 289
 FT TRANSSEM 290 310
 FT TRANSSEM 311 350
 FT CARBOHYD 6 6
 FT CARBOHYD 19 19
 FT DISULFID 112 184
 FT SEQUENCE 350 AA; 39913 MW; BE26049D25757C8 CRC64;

Query Match Best Local Similarity 100.0%; Score 1819; DB 1; Length 350;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
 QY 61 MVAIAIAYKKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVNLGKIMCKITTSALYT 120
 DB 61 MVAIAIAYKKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVNLGKIMCKITTSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVPCMIICFCVMAAAILISIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVPCMIICFCVMAAAILISIPOLVFTVND 180
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVPCMIICFCVMAAAILISIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVPCMIICFCVMAAAILISIPOLVFTVND 180
 QY 181 NARCIPIPRYLGTSMKALIMLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPK 240
 DB 181 NARCIPIPRYLGTSMKALIMLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPK 240
 QY 241 VLTAVVAVFYIYOLPYNVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTALFHSCLNP 300
 DB 241 VLTAVVAVFYIYOLPYNVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTALFHSCLNP 300
 QY 301 ILVYFMGASFKNYMKYKGYSMRROSVEEPPDESGTEPTSTFSI 350
 DB 301 ILVYFMGASFKNYMKYKGYSMRROSVEEPPDESGTEPTSTFSI 350

RESULT 2
 CRRB_BOVIN
 ID CRRB_BOVIN STANDARD; PRT; 350 AA.
 AC P35350;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 11 (C-C CR-11) (CC-CR-11) (CCR-11)
 DE (Possible gustatory receptor type B) (PPR1 protein).
 GN CCR11.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.

RC TISSUE= Tongue; PubMed=8392843;
 RX MEDLINE=93326166; Aoki T., Kurihara K.;
 RA Matsuno I., Mori T., Sato T.,
 RT "Identification of novel members of G-protein coupled receptor
 RT superfamily expressed in bovine taste tissue";
 RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
 CC SCVA19/MIPB/SLC, SCVA21/SLC and SCVA25/TECK (BY SIMILARITY).
 CC -1- FUNCTION: RECEPTOR FOR SCVA2/MCP1, SCVA25/TECK (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
 CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
 CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
 CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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DR EMBL: S63848; AAB27547.1; -
 DR PIR: JN0621; JN0621.
 DR HSSP: P02699; 1BOJ.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PS00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation.
 KW DOMAIN 1 41
 FT TRANSSEM 42 66
 FT TRANSSEM 67 79
 FT TRANSSEM 80 99
 FT TRANSSEM 100 113
 FT TRANSSEM 114 135
 FT TRANSSEM 136 153
 FT TRANSSEM 154 175
 FT TRANSSEM 176 199
 FT TRANSSEM 200 222
 FT TRANSSEM 223 241
 FT TRANSSEM 242 265
 FT TRANSSEM 266 283
 FT TRANSSEM 284 306
 FT TRANSSEM 307 350
 FT CARBOHYD 6 6
 FT CARBOHYD 19 19
 FT DISULFID 112 184
 FT SEQUENCE 350 AA; 40008 MW; E46BP942F3919C82 CRC64;

Query Match Best Local Similarity 89.1%; Score 1620; DB 1; Length 350;
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
 QY 61 MVAIAIAYKKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVNLGKIMCKITTSALYT 120
 DB 61 MVAIAIAYKKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVNLGKIMCKITTSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVPCMIICFCVMAAAILISIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVPCMIICFCVMAAAILISIPOLVFTVND 180
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVPCMIICFCVMAAAILISIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVPCMIICFCVMAAAILISIPOLVFTVND 180
 QY 181 NARCIPIPRYLGTSMKALIMLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPK 240
 DB 181 NARCIPIPRYLGTSMKALIMLEICIGFVVPFLIMGVCFITARTLMKMPNIKISRPK 240


```

CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
CC      LYMPH NODES AND SPLEEN.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      -----
DR      EMBL; U45982; AAA93319.1; -.
DR      Genew; HGNC:1610; CCR9.
DR      MIM: 604738; -.
DR      InterPro: IPR004069; CC_chemkin9.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS; PRO1531; CHEMOKINER9.
DR      PRINTS; PRO0237; GPCR_RHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
FT      DOMAIN 1 37
FT      TRANSMEM 38 64
FT      TRANSMEM 65 73
FT      TRANSMEM 74 94
FT      TRANSMEM 95 108
FT      TRANSMEM 109 130
FT      TRANSMEM 131 148
FT      TRANSMEM 149 169
FT      TRANSMEM 170 198
FT      TRANSMEM 199 226
FT      TRANSMEM 227 242
FT      TRANSMEM 243 268
FT      TRANSMEM 269 292
FT      TRANSMEM 293 310
FT      DOMAIN 311 357
FT      CARBOHYD 20 20
FT      DISULFID 107 186
FT      SEQUENCE 357 AA; 40713 MW; 96982E0B922F6B31 CRC64;
SQ
Query Match 35.0%; Score 637; DB 1; Length 357;
Best Local Similarity 36.5%; Pred. No. 3,4e-32;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4
QY 10 DYVEE-NENNGTYDSOYELICIKEDVREFAKVFLPYELITIVFGLAGNSVAVALYAY 68
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 DYGESESTSMEDYVNFNFDFCEKKNRQSFASHPLEPLVYLVEIFVGLANSSTLIAYWY 63
QY 69 YKKQRTFTDYIILNLAADLLFLPLFAVAVAVGWLGIMCKIKISALYTLNPFVSGQ 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 CTRKRTITDDEFLNLAIDLPLVTLPEWALAADQMFQTPCKVNVSMKMFVSCVL 123
QY 129 FLACISIDRVAATKTPSOSGVGKPCW-----IICFCVMAATILSIPOLVETYN 179
   : |||:||||:| | | | | | | | | | | | | | | | | | | | | | | |
Db 124 LIMISIDRIVAIAQ-----AMRAHTRMRKRLYSKMWCFITVLAALACIPELVSQIK 178
QY 180 DN--ANCPIDIEPRVYLGTSKALIQMLELTCIGFVVPFLMGVCYFITARPLMKPNKIS 236
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 179 EESGIALCTWVYSDSTKLSKSAVLTLKVLILGELFPLFVMAVCYTIIHRLIOAKRSSKH 238
QY 237 RPLKVLITVTVIVTQOLPYNTVKRCRAIDILYSLTSCNNKSRKADIAVOTESIALFHS 296
   : |||:||||:| | | | | | | | | | | | | | | | | | | | | | | |
Db 239 KALKVITVTVLVVTSQFPNCLILVQTDIATAMFISCAVSTINDICFOYTQIAPFHS 298
QY 297 CLNPILVYVFGASFKNYVMKVAKKYG 322
   |||:||||:| | : : | | |
Db 299 CLNPILVYVFGERPRDLVKTLLNG 324

```

CKR6_MOUSE STANDARD: PRT: 367 AA.

AC 054689; 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C Chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (KYL11).

GN CCR6 OR CCR6B.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Yanagihara S., Komura E., Yamaguchi Y.;

RT "Mouse G protein-coupled receptor KY411."

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=9077268; PubMed=9862452;

RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,

RA Albar J.P., Ardevin C., Marquez G.;

RT "Molecular cloning, functional characterization and mRNA expression

RT analysis of the murine chemokine receptor CCR6 and its specific ligand

RT MIP-3alpha."

RL FEBS Lett. 440:188-194(1998).

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-

CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE

CC INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: AB009369; BAA23776.1; -

DR EMBL: AJ222714; CAI10956.1; -

DR MGD: MGI:1333797; Cmkdr6.

DR InterPro: IPR004067; CC-Chemokine6.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PRO1529; CHEMOKINER6.

DR PRINTS: PRO0237; GPCRHOOPS.

DR PROSITE: PS00237; G-PROTEIN RECP_FL1; 1.

DR PROSITE: PS50262; G-PROTEIN RECP_FL2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 39

FT TRANSMEM 40 66

FT DOMAIN 67 75

FT TRANSMEM 76 96

FT DOMAIN 97 111

FT TRANSMEM 112 133

FT DOMAIN 134 151

FT TRANSMEM 152 172

FT DOMAIN 173 203

FT TRANSMEM 204 230

FT TRANSMEM 231 246

FT TRANSMEM 247 271

FT TRANSMEM 272 295

FT TRANSMEM 296 313

FT DOMAIN 314 367

FT DISULFID 110 189

FT CARBOHYD 2 2

FT CARBOHYD 35 35

SO SQUENCE 367 AA; 42102 MW; 6A309A83B1117E CRC64;

Query Match 33.3%; Score 605; DB 1; Length 367;

Best Local Similarity 37.9%; Pred. No. 3e-30;

Matches 129; Conservative 60; Mismatches 125; Indels 26; Gaps 8;

QY 8 STDYEEENMNGTQDYSOYELI-----CIKEDYREFAKVLPVFLIVFVIGLAGNSM 61

DB 3 STEYSGTGD-----IDNTETYSIPDPHGPCSLEEBRNFTKVFVPLAYSILCYFGLGIM 58

QY 62 VVAIYAVYKQKPTDVIYLLNAVADLLFLTPMAV-NAVHGVLGKIMCKITSLALT 120

DB 59 VVMTFAFYKARSMGTDVYLLNMAIDILFVLTPMAVTHATNTVWFSDALCKLKKGYA 118

QY 121 LNFVSMQFLACISIDRYAVATKVPSSQSGVKPC-----IICFCVMAAILSLQVLF- 175

DB 119 VVNCGMILLACISMDRYAIVQATKSRVRSRTLTSHSKVAVFISIISSPTFLN 178

QY 176 --YVVDNARCIPFPYRYLGTG---MKALQMLEICGFVFPFLMGVCYFRTATLMK 229

DB 179 KYEELDRVC---EPRVRSVSEPTWKLGLGELFFGFTPLFMVFCYLIKITLVQ 235

QY 230 MPNIKISPLKVLVIVIVIVITOLPYNIVKFCRAIDIIYSLITSCNNSKRMDIAIOYTE 289

DB 236 AONSKRHRAIRVIAVIVIFLACQIPHNVLVTAVN-TGKVGRCSTEKVLAATRVAV 294

QY 290 STALFSCINPLIYVEMGASFKNYMKVAKKGRQRQ 329

DB 295 VLAFLHCLNPLVLAFLIGQKERNYEMKIMKIDVCMRRKNK 334

RESULT 8

CKR6_HUMAN STANDARD: PRT: 374 AA.

AC P51684; Q92846; P78533;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C Chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC

DE receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CCR-L3)

DE (DRY6).

GN CKR6 OR CCKBR6 OR STRL22 OR GPR29 OR CKRL3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND FUNCTION.

RA MEDLINE=97313465; PubMed=9169459;

RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,

RA Nomiyama H., Yoshie O.;

RT "Identification of CCR6, the specific receptor for a novel

RT lymphocyte-directed CC chemokine LARC."

RL J. Biol. Chem. 272:14893-14898(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Laurens L.L., Modi W., Bonner T.I.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA MEDLINE=97040707; PubMed=8886020;

RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;

RT "Molecular cloning and RNA expression of two new human chemokine

RT receptor-like genes."

RL Biochem. Biophys. Res. Commun. 227:846-853(1996).

RN [4]

RP SEQUENCE FROM N.A.

RA McCoy R., Perlmutter D.H.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA MEDLINE=97224503; PubMed=9070937;

RA Liao F., Lee H.-H., Farber J.M.;

RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled

RT receptor related to chemokine receptors and located on chromosome

RT 6q27."

RL Genomics 40:175-180(1997).


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CC TRANSMEM 188 215 5 (POTENTIAL).
CC DOMAIN 216 231 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 232 259 6 (POTENTIAL).
CC DOMAIN 260 275 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 276 293 7 (POTENTIAL).
CC DOMAIN 294 342 CYTOPLASMIC (POTENTIAL).
CC DISULFID 102 180 BY SIMILARITY.
CC CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;

Query Match 31.9%; Score 581; DB 1; Length 342;
Best Local Similarity 34.2%; Pred. No. 8,1e-29;
Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps 8;

QY 12 YEEENMGTYDSQYELICIKEDVREFAFVLPFLTVIVIGLAGNSMVAIYAYK 71
DB 6 HYEDGFGFNSDSE-----HDFLOFRKVFPCMLVAVVCGVLSVLVSIYK 61

QY 72 QRTKTDVYIILAVADLLFTLPMAVNAVHGVNLKIMCKITSALTYNFSGMFLA 131
DB 62 LQSLDVFVNLPLADLVFVCTLPFMAVAGIHEWIFGVCKTLGLTYTINFTSMILT 121

QY 132 CISIDRYVAATKVP--QSGVGKPCW--IICFCVMAAILISTPOLVFTV--NDNARCI 185
DB 122 CTYDRTFVAVKATKAVNQAKMTGKVICLLIWTIVLSLVSQIITIGVNFENLDKLC- 180

QY 186 PIFPRYLGTSKALIMLEICIGFVVPFLMGVCYFTIARTLMKPNIKISRPLKVLTV 245
DB 181 ----GYHDEEISTVLAOTMTLGFELPLAMIVCYSVIITKLHAGGFQKHSKLTIFLV 236

QY 246 VIVFIVTQLPYNIYKFCRAIDIIYSLTSCNMSKRMIDAIQVTSIALFHSCLNPIIYV 305
DB 237 MAVFLLTQTPENLVKLRSTHMEYAMTSFHYT-----IIVTEALVLRACLPVLYAF 290

QY 306 MGASEKNYVMVAKKYG-----SWRROROSVEEPFDSKPTSTFSI 350
DB 291 VSLKFRKFNKLVKIDIGCLPYLGVSQKSSSDNSK--TFSASHNVEATISMFL 342

RESULT 10
CCR6_MACMU STANDARD; PRT; 343 AA.
AC 09XTA5;
DB 16-OCT-2001 (Rel. 40, Created)
DB 16-OCT-2001 (Rel. 40, Last sequence update)
DB 15-JUN-2002 (Rel. 41, Last annotation update)
DB C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
DE receptor bonzo) (G protein-coupled receptor STRL33).
CN CXCR6 OR BONZO OR STRL33.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21354176; Pubmed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
CC CORRECTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC EMBL: AF124380; AAD31419.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
DR DISULFID 102 180 BY SIMILARITY.
CC CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 31.4%; Score 571; DB 1; Length 343;
Best Local Similarity 33.4%; Pred. No. 3,3e-28;
Matches 119; Conservative 73; Mismatches 132; Indels 32; Gaps 8;

QY 10 DYEEENMGTYDSQYELICIKEDVREFAFVLPFLTVIVIGLAGNSMVAIYAYK 69
DB 5 DYEDGFGFNSDSE-----HDFLOFRKVFPCMLVAVVCGVLSVLVSIYK 60

QY 70 KQRTKTDVYIILAVADLLFTLPMAVNAVHGVNLKIMCKITSALTYNFSGMFL 129
DB 61 HKLQSLDVFVNLPLADLVFVCTLPFMAVAGIHEWIFGVCKTLGLTYTINFTSMILT 120

QY 130 CISIDRYVAATKVP--QSGVGKPCW--IICFCVMAAILISTPOLVFTV--NDNAR 183
DB 121 LQSLDVFVNLPLADLVFVCTLPFMAVAGIHEWIFGVCKTLGLTYTINFTSMILT 180

QY 184 CIPFPRYLGTSKALIMLEICIGFVVPFLMGVCYFTIARTLMKPNIKISRPLKVL 243
DB 181 ----GYHDEEISTVLAOTMTLGFELPLAMIVCYSVIITKLHAGGFQKHSKLTIF 235

QY 244 TYVIVTQLPYNIYKFCRAIDIIYSLTSCNMSKRMIDAIQVTSIALFHSCLNPIIY 303
DB 236 LVMAVFLLTQTPENLVKLRSTHMEYAMTSFHYT-----IIVTEALVLRACLPVLY 289

QY 304 VEMGASEKNYVMVAKKYG-----SWRROROSVEEPFDSKPTSTFSI 350
DB 290 AFVSLKFRKFNKLVKIDIGCLPYLGVSQKSSSDNSK--TFSASHNVEATISMFL 343

RESULT 11
CCR6_MACMU STANDARD; PRT; 342 AA.
AC 019024;
DB 15-JUL-1998 (Rel. 36, Created)
DB 15-JUL-1998 (Rel. 36, Last sequence update)
DB 15-JUN-2002 (Rel. 41, Last annotation update)
DB C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
DE receptor bonzo).
CN CXCR6 OR BONZO.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97373958; PubMed=9230441;
 RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
 RT "Expression cloning of new receptors used by simian and human
 immunodeficiency viruses.";
 RL Nature 388:296-300(1997).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
 CC CORECEPTOR BY STVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: AF007858; AAB64224.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32
 FT TRANSMEM 33 59
 FT DOMAIN 60 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 103
 FT TRANSMEM 104 125
 FT DOMAIN 126 143
 FT TRANSMEM 144 164
 FT DOMAIN 165 187
 FT TRANSMEM 188 215
 FT DOMAIN 216 231
 FT TRANSMEM 232 259
 FT DOMAIN 260 275
 FT TRANSMEM 276 293
 FT DOMAIN 294 342
 FT DISULFID 102 180
 FT CAROHND 16 16
 SQ SEQUENCE 342 AA; 39297 MW; 55F9F68CB62DD2D5 CMC64;
 N-LINKED (GLCNAC...) (POTENTIAL).
 Query Match 31.3%; Score 569; DB 1; Length 342;
 Best Local Similarity 33.6%; Pred. No. 4.3e-28;
 Matches 119; Conservative 72; Mismatches 131; Indels 32; Gaps 8;

RESULT 12
 ID CCR6_HUMAN STANDARD; PRT; 342 AA.
 AC 000574; 000575;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
 DE receptor homoz) (G protein-coupled receptor STRL33).
 GN CXCR6 OR BONZO OR STRL33 OR TYMSR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97373958; PubMed=9230441;
 RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
 RT "Expression cloning of new receptors used by simian and human
 RT immunodeficiency viruses.";
 RL Nature 388:296-300(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97311099; PubMed=9166430;
 RA Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A.,
 RA Farber J.M.;
 RT "STRL33, A novel chemokine receptor-like protein, functions as a
 RT fusion cofactor for both macrophage-tropic and T cell line-tropic
 RT HIV-1.";
 RL J. Exp. Med. 185:2015-2023(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97431687; PubMed=9285716;
 RA Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
 RA Baggiolini M., Arenzana-Seisdedos F., Moser B.;
 RT "TYMSR, a putative chemokine receptor selectively expressed in
 RT activated T cells, exhibits HIV-1 coreceptor function.";
 RL Curr. Biol. 7:652-660(1997).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A
 CC CORECEPTOR BY STVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T
 CC CELLS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL: AF007545; AAB64221.1;
 DR EMBL: U73529; AAB61456.1;
 DR EMBL: U73531; AAB61457.1;
 DR EMBL: Y13248; CAA73698.1;
 DR MIM: 605163;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 FT DOMAIN 1 32
 FT TRANSMEM 33 59
 FT DOMAIN 60 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 103
 FT TRANSMEM 104 125
 FT DOMAIN 126 143
 CYTOPLASMIC (POTENTIAL).


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FT TRANSMEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 142 3 (POTENTIAL).
FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 183 4 (POTENTIAL).
FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 231 5 (POTENTIAL).
FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 252 273 6 (POTENTIAL).
FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 119 196 BY SIMILARITY.
SQ SEQUENCE 360 AA; 40759 MW; 564F04ABBC0A197 CRC64;

Query Match 29.4%; Score 534.5; DB 1; Length 360;
Best Local Similarity 33.2%; Pred. No. 5.5e-26;
Matches 120; Conservative 75; Mismatches 141; Indels 25; Gaps 8;

QY 3 LEONOSTDYEEENEMNGTYDSQYELI-----CIKEDVREFAKVFLPFLTIIVIGLA 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 6 MESDSFEDFMKGEDLSNYSYSTLPFLDAPCEPESL-EINKYFVITVALVFLSL 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 GNSWVAIYAYKKORTDYIILNLAVALLLFTLPFMAVNAHGWYGLKIMCKITSA 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 65 GNSLWLVILSVRSVSTVDYLLNLADLFTLPIMASKVNGMIFGTFLKVVSL 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 LYTLPFVSGMQLACISIDRYAVV---TKVPSOGVGKPCWITFCVMAAILISIPOLV 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 125 LKEVNFYSGLILACISIDRYALVHARTLTQKRY--LVKFCILSIMGSLALLPVL 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 F---YVNDNARCIPIFRYLG---TSMKALIMLEICIGVFPFLMGVCFITARTL 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 FRRYVSSNVSPAC---EDMGNNNTAMWMLRLPQSESEFVPLIMLFCYFTLRTL 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 228 MKMPNIRKISRPKLVLTIVYVITQLPYNIYKFCRAIDIIYLSITSCNMSKRDIAIOV 287
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 239 FKAHMGQKRRAMRVFAVVLFTLCMLPYNLVTLADTLMTROYIOECERNRHIDRLADA 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 288 TESIALFHSCLNPLIYVFMGASFKNYKVAKYGSMNRQ---RQSYEEFPDESGTPT 344
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 299 TELIGILHSCNPLIYAFIGQKFRHGLKILAIHGLISKDSLKPSDRSPVSGSSGHTST 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 345 T 345
   :
DB 359 T 359

RESULT 15
IL8B_PANTR 1L8B_PANTR STANDARD; PRT; 353 AA.
AC Q28807;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE High affinity Interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).
GN IL8RB OR CXCR2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OC NCBI_TaxId=9598;
RX MEDLINE=96175151; Pubmed=9110929;
RA Alvarez V., Coto E., Sellen F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Latre C.;
RA "Characterization of interleukin-8 receptors in non-human primates.";
RA Immunogenetics 43:261-267(1996).
CC -I- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND

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CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC EMBL: X91113; CA62563.1; -.
CC HSSP: P34996; 1DDD.
DR InterPro: IPR000276; GPCR_Rhodospn.
DR InterPro: IPR000832; GPCR_secretin.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPE_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT NON_TER 1 1
FT TRANSMEM 46 72 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 73 81 1 (POTENTIAL).
FT TRANSMEM 82 102 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 103 117 2 (POTENTIAL).
FT TRANSMEM 118 139 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 140 160 3 (POTENTIAL).
FT TRANSMEM 161 180 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 181 205 4 (POTENTIAL).
FT TRANSMEM 206 228 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 229 248 5 (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT TRANSMEM 271 291 7 (POTENTIAL).
FT TRANSMEM 292 312 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 29.1%; Score 529.5; DB 1; Length 353;
Best Local Similarity 33.6%; Pred. No. 1.1e-25;
Matches 118; Conservative 74; Mismatches 132; Indels 27; Gaps 8;

QY 3 LEONOSTDYEEENEMNGTYDSQYELI-----CIKEDVREFAKVFLPFLTIIVIGLA 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 3 MESDSFEDFMKGEDLSNYSYSTLPFLDAPCEPESL-EINKYFVITVALVFLSL 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 GNSWVAIYAYKKORTKDYIILNLAVALLLFTLPFMAVNAHGWYGLKIMCKITSA 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 GNSLWLVILSVRSVSTVDYLLNLADLFTLPIMASKVNGMIFGTFLKVVSL 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 LYTLPFVSGMQLACISIDRYAVV---TKVPSOGVGKPCWITFCVMAAILISIPOLV 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 122 LKEVNFYSGLILACISIDRYALVHARTLTQKRY--LVKFCILSIMGSLALLPVL 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 175 F---YVNDNARCIPIFRYLG---TSMKALIMLEICIGVFPFLMGVCFITARTL 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 180 FRRYVSSNVSPAC---EDMGNNNTAMWMLRLPQSESEFVPLIMLFCYFTLRTL 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 228 MKMPNIRKISRPKLVLTIVYVITQLPYNIYKFCRAIDIIYLSITSCNMSKRDIAIOV 287
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 236 FKAHMGQKRRAMRVFAVVLFTLCMLPYNLVTLADTLMTROYIOETCERRRHIDRLADA 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 288 TESIALFHSCLNPLIYVFMGASFKNYKVAKYGSMNRQSYEEFPDESGTPT 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 296 TELIGILHSCNPLIYAFIGQKFRHGLKILAIHGLISKDSLKPSDRSPVSGSSGHTST 341
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: March 14, 2003, 16:11:45

Mon Mar 17 12:24:55 2003

us-09-686-020a-2.rsp

Page 13

Job time : 13 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:10:47 ; Search time 19 Seconds
(without alignments)
1770.897 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEQNSTDYEEENMNG.....VEEPFDSGPTPTSTFST 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR_73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------------------------|
| 1 | 1620 | 89.1 | 350 | 2 JN0621 | G protein-coupled lymphocyte-specific |
| 2 | 650 | 35.7 | 378 | 2 A55735 | G protein-coupled |
| 3 | 643 | 35.3 | 378 | 2 A45680 | G protein-coupled |
| 4 | 583 | 32.1 | 369 | 2 JC5068 | chemokine (C-C) re |
| 5 | 537.5 | 29.5 | 360 | 2 A57160 | interleukin-8 rece |
| 6 | 534.5 | 29.4 | 360 | 2 A53611 | probable G protein-c |
| 7 | 524 | 28.8 | 354 | 2 J58186 | orphan G protein-c |
| 8 | 522.5 | 28.7 | 360 | 2 JC4304 | chemokine (C-C) re |
| 9 | 522.5 | 28.7 | 360 | 2 JC4587 | G protein-coupled |
| 10 | 518.5 | 28.1 | 354 | 2 B55733 | interleukin-8 rece |
| 11 | 511 | 28.1 | 358 | 2 A53752 | neuropeptide Y/pep |
| 12 | 501.5 | 27.6 | 355 | 2 JQ1231 | neuropeptide Y/pep |
| 13 | 500.5 | 27.5 | 352 | 2 A45747 | neuropeptide Y/pep |
| 14 | 499.5 | 27.1 | 353 | 2 S28787 | neuropeptide Y/pep |
| 15 | 493.5 | 27.1 | 352 | 2 G00048 | chemokine (C-C) re |
| 16 | 492.5 | 27.0 | 360 | 2 JC2443 | chemokine (C-C) re |
| 17 | 489.5 | 26.9 | 350 | 2 A39445 | G protein-coupled |
| 18 | 486 | 26.7 | 355 | 2 JC5067 | macrophage inflamm |
| 19 | 485 | 26.6 | 355 | 2 A43339 | chemokine (C-C) re |
| 20 | 484.5 | 26.6 | 352 | 2 A43113 | interleukin-8 rece |
| 21 | 483.5 | 26.6 | 359 | 2 A48921 | chemokine (C-C) re |
| 22 | 482 | 26.5 | 374 | 2 I38450 | chemokine (C-C) re |
| 23 | 479.5 | 26.4 | 359 | 2 I49341 | MIP-1 alpha recept |
| 24 | 476.5 | 26.2 | 367 | 2 JE0349 | interferon-inducib |
| 25 | 474 | 26.1 | 355 | 2 A45177 | chemokine (C-C) re |
| 26 | 471 | 25.9 | 356 | 2 S42096 | interleukin-8 rece |
| 27 | 470 | 25.8 | 383 | 2 S55594 | G protein-coupled |
| 28 | 461.5 | 25.4 | 355 | 2 G02436 | chemokine (C-C) re |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 455.5 | 25.0 | 359 | 2 S44425 | angiotensin II rec |
| 31 | 452.5 | 24.9 | 359 | 2 JC1104 | angiotensin II rec |
| 32 | 452.5 | 24.9 | 359 | 2 JC2134 | angiotensin II rec |
| 33 | 450 | 24.7 | 359 | 2 S15403 | angiotensin II rec |
| 34 | 450 | 24.7 | 374 | 2 S32785 | G protein-coupled |
| 35 | 446.5 | 24.5 | 359 | 2 A48857 | angiotensin II rec |
| 36 | 445.5 | 24.5 | 356 | 2 I49340 | MIP-1 alpha recept |
| 37 | 442.5 | 24.3 | 372 | 2 S26667 | G protein-coupled |
| 38 | 442.5 | 24.3 | 374 | 2 S42628 | G protein-coupled |
| 39 | 441 | 24.2 | 362 | 2 JN0694 | angiotensin II rec |
| 40 | 439 | 24.1 | 359 | 2 A42656 | angiotensin II rec |
| 41 | 438.5 | 24.1 | 359 | 2 JH0621 | angiotensin II rec |
| 42 | 438.5 | 24.1 | 362 | 2 A39714 | G protein-coupled |
| 43 | 437.5 | 24.1 | 327 | 2 S56162 | MDCR15 protein - h |
| 44 | 434 | 23.9 | 359 | 2 J01516 | angiotensin II rec |
| 45 | 428.5 | 23.6 | 359 | 2 I39418 | angiotensin II rec |

ALIGNMENTS

RESULT 1

JN0621
G protein-coupled receptor type B - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
C:Accession: JN0621
R:Matsuroka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K. ;
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A:Title: Identification of novel members of G-protein coupled receptor superfamily ex
A:Reference number: JN0621; MUID:93326166; PMID:8392843
A:Accession: JN0621
A:Molecule type: mRNA
A:Residues: 1-350 <MAT>
A:Cross-references: GB:563848; NID:9399710; PIDN:AAB2547.1; PID:9399711
A:Experimental source: tongue taste papillae
C:Comment: This protein is involved in modulating taste sensitivity or regeneration o
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
F:42-66/Domain: transmembrane #status predicted <TM1>
F:80-99/Domain: transmembrane #status predicted <TM2>
F:114-135/Domain: transmembrane #status predicted <TM3>
F:154-175/Domain: transmembrane #status predicted <TM4>
F:200-222/Domain: transmembrane #status predicted <TM5>
F:242-265/Domain: transmembrane #status predicted <TM6>
F:284-306/Domain: transmembrane #status predicted <TM7>
F:6.19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 1,3e-131;

Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MALEQNSTDYEEENMNGTYSOVELCTIEDREFKAVLPVFTVFVIGLAGNS | 60 |
| DB | 1 | MAVEYNSTDYEEENMNDTHDSOTEVCTKEERKFAKVLPAFPFTAFITGLAGNS | 60 |
| QY | 61 | MVAIVAYVYKKRKRTDVTLLNLAVALDLLFTLPFMAVAVAGVVGKIMCKTSALYT | 120 |
| DB | 61 | TVAIVAYVYKKRKRTDVTLLNLAVALDLLFTLPFMAVAVAGVVGKIMCKTSALYT | 120 |
| QY | 121 | LNFVSGQFLACISIDRYAVAVTKVPSSGSGKRCMTICFCVMAAIIISLPOLVFTVND | 180 |
| DB | 121 | VNFVSGQFLACISIDRYAVAVTKVPSSGSGKRCMTICFCVMAAIIISLPOLVFTVND | 180 |
| QY | 181 | NACGIPFEPYVLTGSMKALITOMLETCGFVPPPLINGVCFIARTLMMKPNKISRPLK | 240 |
| DB | 181 | KACVPIFPYHLDGSMKASITQILEICGFIPLPMAVCFITAKTLIMKPNKISRPLK | 240 |
| QY | 241 | VLLTVVIVFTVQLPYNIYFCRAIDIIYSLITSCNMSKMDIAIVTSTIAFHSCLNP | 300 |
| DB | 241 | VLLTVVIVFTVQLPYNIYFCRAIDIIYSLITSCNMSKMDIAIVTSTIAFHSCLNP | 300 |
| QY | 301 | ILVYFGASFKRYVMKAYKGYGSMRRQSGVEEPFDSGPTPTSTFST 350 | |

```
Db      301 VLVEFMGTSFKNYIMKYAKKGSWRQQRNVEEIPFESEDATEPTSTFSI 3500
```

RESULT 2

Lymphocyte-specific G protein-coupled receptor EB11 - human
 N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
 C:Species: Homo sapiens (man)
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
 C:Accession: B55735; #accession_revision 07-Jul-1995 #text_change 19-May-2000
 R:Schweickart, V.L.; Rapoport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A:Reference number: A55735; MUID:95154835; PMID:7851893
 A:Accession: B55735
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-378 <SCCH>
 A:Cross-references: GB:J1581; NID:g468319; PID:AAA74231.1; PID:g468320
 R:Burgstahler, R.; Kempkes, B.; Staebke, K.; Lippe, M.
 submitted to the EMBL Data Library, February 1995
 A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically transe
 A:Reference number: S52443
 A:Accession: S52443
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 21-378 <BUR>
 A:Cross-references: EMBL:X84702
 C:Genetics:
 A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
 A:Cross-references: GDB:342065; OMIM:600242
 A:Map position: 17q12-17q21.2
 A:Superfamily: vertebrate rhodopsin
 A:Keywords: G protein-coupled receptor

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 36.2%; | Score 659; | DB 2; | Length 378; |
| Best Local Similarity | 38.7%; | Pred. No. 4.8e-49; | | |
| Matches 144; | Conservative 66; | Mismatches 124; | Indels 38; | Gaps 77; |

[illegible]

RESULT 3
A55735
G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweilokatt, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB1, a lymphoid-specific G-protein-coupled recep
A:Reference number: A55735; MUID:95154835; PMID:7851893
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SC>
A:Cross-references: GB:L1580; NID:g468340; PIDN:AAA7423.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 35.7% | Score 650; | DB 2; | Length 378; |
| Best Local Similarity | 38.3% | Pred. No. 2.8e+48; | | |
| Matches 140; | Conservative 67; | Mismatches 125; | Indels 34; | Gaps 8; |

```

OY      5 ONOSDYVEENENMGTYDASQYELICIKEDVREFAKFLPEVFLTFVFIAGNSWVA 64
Db      25 ODEWTDYIGENT---IYDTLYLESYCEKKDYRNFKAMFLPLMVSVCPEGLLNGVL 81
OY      65 IYAYYKQRTFDYVILNLAVADLLLETPFMVAHVHGVNLCKIMCKITTSALTYLNEV 124
Db      82 TYIYEFRLKRTDGYLLNLAAVDLLLETPFMAYSEAKSIFGVYLCKGIFGIKLSF 141
OY      125 SGMQFLACISIDRYVATYKVSQS-----VKPCMIICFCWMAAILLSIPOLYFTT 177
Db      142 SGMELLLCISIDRYVAIYQAVSRHRHARVLLISK---LSCVGLMMLALPLSLPELlySG 198
OY      178 VNDNA-----RCIFLPRYLTSKAL--IOMLEICIGFVVPFLMGCVFIARTLTMK 230
Db      199 LQKNSGDTLNC-----SLSAQYVALITTOVQOMVGFVPLMLAMSFCLIIIRILLQA 253
OY      231 PNKISRDLKVLVIVIVEITQLPYIVAFCAIDIIYSITSCNSKRMIDAIOVTES 290
Db      254 RNFERNKAIKVIIVAVVVEVIFQEPNGVYLAQVAVANFNITNSSCERSKQNLIAVDYTS 313
OY      291 IALFHSCLNPLLYFPMGASFKNYMKYAKKYGSMRROR-----QSVEEPDSDSPT 343
Db      314 LASVRCVNPFLYAFIGVKFRSDLFKLDGLCSOERLHRHWSCHRYNARSVSM--AE 371
OY      344 PTSTFS 349
Db      372 TTTFES 377

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RESULT 4
A:Accession: A45680
G:protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenciol, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled
A:Reference number: A45680; MUID:93188173; PMID:8363238
A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BIR>
A:Cross-references: GB:L08176; NID:q183484; PID:q183485
A:Experimental source: GB:L08176; NID:q183484; PID:q183485
A>Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIPI:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

```

```

Query Match:          35.3%; Score 643; DB 2; Length 376;
Best Local Similarity 39.0%; Pred. No. 1,1e-47;
Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

OY      1 MALEQMSDDYYEENMGTYDSQVLLICKEDVAFKAVLPVFLTIVPIGLAGNS 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

QY 1 MALEQNOSTDYEEENEMNGTIDYSOYELLCICKEDVREFAKVPFLPYELTVIVIGLAGNS 600
 : |::|·|·| | ||:::||:|||| | ||:: ::: ||||

Db 21 VCLCODEVTDYIDGNT---TVDYTFESLCSKRDVNFKAMELPIMYSIICEVGLGNG 77
 QY 61 MVVAIYAYKKORRTDYIILNVAADLLFTLPFMAVNAHVGWLGKIMCKITSAIYT 120
 Db 78 LVVLTITFKRKRTMTDYILNVAADLLFTLPFMAVNAHVGWLGKIMCKITSAIYT 137
 QY 121 LNFVSGMOFLACISIDRYVAATKVSQSGVKPCMI--CFVWMA--AIIISTIPOLVFY 176
 Db 138 MSFSGMILLICISIDRYVAATKVSQSGVKPCMI--CFVWMA--AIIISTIPOLVFY 197
 QY 177 TVNDA-----RCIPIFRYLGTSKMAIOMLEICIGFVPELIMGVCFYFARTLMMKP 231
 Db 198 DLQRSSSQAMKCSLITEH---VEAFITIOVAQWITGFLVPELIMGVCFYFARTLMMKP 254
 QY 232 NIKIRSRPLKVLTVYIVFVITQLPYNIYFCRAIDIIYSLTSCMSKRDIAIOVTESTI 291
 Db 255 NERKKAIVITAVVVFVIFQLPYNGVLAQTVANFNITSTCHLSKQIINADVTSYL 314
 QY 292 ALPHSCNPLILYFVGASRKNYVMVAKKYG-----SW-----RROQSVPEFPFD 337
 Db 315 ACVRCVNPFLYAFIVGFRNDIFKFLKDLGCLSOEQLRQMSCKRHIRRSKSYE----- 369
 QY 338 SEGPTPTSTFS 349
 Db 370 ----AETTTTFS 377

RESULT 5

JC5068
 G protein-coupled receptor CRK-L3 - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C:Accession: J03068
 R:Fabbllos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
 A:Reference number: JC5067; MUID:97040707; PMID:886020
 A:Accession: J03068
 A:Molecule type: DNA
 A:Residues: 1-369 <ZAB>
 A:Cross-references: EMBL:279784; NID:91668737; PIDN:CA02144.1; PID:91668738
 C:Comment: This protein belongs to the family of alpha chemokine receptors.
 C:Genetics:
 A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CRK-L3; GPR-CY4
 A:Cross-references: GDB:5370639; OMTM:601835
 A:Map position: 6q27-6q27
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:42-68/Domain: transmembrane #status predicted <TM1>
 F:79-99/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:160-180/Domain: transmembrane #status predicted <TM4>
 F:212-233/Domain: transmembrane #status predicted <TM5>
 F:250-271/Domain: transmembrane #status predicted <TM6>
 F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 32.1%; Score 583; DB 2; Length 369;
 Best local similarity 36.1%; Pred. No. 1.6e-42;
 Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;

QY 8 STDYIYENENMGTYDYSEYELICIKEDVREPAKFLPVLITVYFVIGLAGNSVVAIYA 67
 Db 18 NTSYYSVDESE-----LICSIOEVRKPSRLPEVPIYSLVCFGLGNTLVITTEA 67
 QY 68 YKKORRTDYIILNVAADLLFTLPFMAVNAHVGWLGKIMCKITSAIYT 126
 Db 68 FYKARSMTDYIILNVAADLLFTLPFMAVNAHVGWLGKIMCKITSAIYT 127
 QY 127 MQLACISIDRYVAATKVSQSGVKPCMI--CFVWMA--AIIISTIPOLVFY 179
 Db 128 MLLTICISIDRYVAATKVSQSGVKPCMI--CFVWMA--AIIISTIPOLVFY 187
 QY 180 DNACIPIFRYLGTSKMAIOMLEICIGFVPELIMGVCFYFARTLMMKP 235

Db 188 GSDVC---EKRYQVSEPIFRKMLMGLELLEFFILPMFMICYFYKTIYVAQNSKR 244
 QY 236 SRPLKVLTVYIVFVITQLPYNIYFCRAIDIIYSLTSCMSKRDIAIOVTESTI 295
 Db 245 HKAIRVIAVVLVAFVLAQIPIHNVLLVTAAN-LGKNRNSQSEKILGYRTYEVLAFLH 303
 QY 296 SCNPLIYVFMGASFKKNYVMVAKKYGSRROKOS 330
 Db 304 CCLNPVLAFTIGOKFRNIFLTKDLKMCVKKIKS 338

RESULT 6

A57160
 Chemokine (C-C) receptor 4 - human
 N:Alternate names: C-C CRK-4
 C:Species: Homo sapiens (man)
 C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: A57160
 R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
 J. Biol. Chem. 270, 19495-19500, 1995
 A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor
 A:Reference number: A57160; MUID:95370289; PMID:7642634
 A:Accession: A57160
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-360 <POW>
 A:Cross-references: GB:X85740; NID:91370103; PIDN:CAA59743.1; PID:9971452
 A:Note: source clone K5-5
 C:Genetics:
 A:Gene: GDB:CMKBR4
 A:Cross-references: GDB:677463
 A:Map position: 3p21-3p21
 C:Superfamily: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
 F:40-65/Domain: transmembrane #status predicted <TM1>
 F:76-97/Domain: transmembrane #status predicted <TM2>
 F:112-133/Domain: transmembrane #status predicted <TM3>
 F:151-175/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:243-264/Domain: transmembrane #status predicted <TM6>
 F:291-308/Domain: transmembrane #status predicted <TM7>
 F:329-376/Domain: transmembrane #status predicted
 F:29-376/Domain: transmembrane #status predicted
 F:72-350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predi
 F:143/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
 F:183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi

Query Match 29.5%; Score 537.5; DB 2; Length 360;
 Best local similarity 35.8%; Pred. No. 1.2e-38;
 Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

QY 10 DYIYENENMGTYDYSEYELICIKEDVREPAKFLPVLITVYFVIGLAGNSVVAIYA 69
 Db 8 DTLDESIYNNYLVESIPKCTKGIKAFGLFPLPSLVFVGLGNSVVAIYLFKY 67
 QY 70 KKKORRTDYIILNVAADLLFTLPFMAVNAHVGWLGKIMCKITSAIYT 129
 Db 68 KKRIRSTDYIILNVAADLLFTLPFMAVNAHVGWLGKIMCKITSAIYT 127
 QY 130 LACISIDRYVAATKVSQSGVKPCMI--CFVWMA--AIIISTIPOLVFY 179
 Db 128 VMLMSIDRLALVAVFSRLARTLYG-----ITSATWSVAVPASPGLFSTCYTER 182
 QY 180 DNACIPIFRYLGTSKMAIOMLEI-CIGFVPELIMGVCFYFARTLMMKP 238
 Db 183 NHTYCKTKYS--LNSYTWKVLSSLEINILGLVILPGLMFCSMIRTLQHCNKKAKNA 240
 QY 239 LKVLITVYIVFVITQLPYNIYFCRAIDIIYSLTSCMSKRDIAIOVTESTI 298
 Db 241 VKMIRAVVVLVAFVLAQIPIHNVLLVTAAN-LGKNRNSQSEKILGYRTYEVLAFLH 303
 QY 299 NPLIYVFMGASFKKNYVMVAKKYGSRROKOS 319

DB 300 NPITVFLGKFRKRYLLQLFK 320

RESULT 7

interleukin-8 receptor type B - human

C:Species: Homo sapiens (man)

C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999

C:Accession: J37898; J38712; A53611; A39446

R:Aluja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 269, 26381-26389, 1994

A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor type B

A:Reference number: J37898; MUID:95014476; PMID:7929358

A:Accession: J37898

A:Molecule type: DNA

A:Residues: 1-360 <RES>

A:Cross-references: EMBL:U11869; NID:9511801; PIDN:AA60656.1; PID:9511803

A:Accession: J38712

A:Molecule type: mRNA

A:Residues: 1-15 <RES>

A:Cross-references: EMBL:U11872; NID:9511808; PIDN:AA64380.1; PID:9511809; EMBL:U11873; NID:9511816; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878; NID:9511819; EMBL:U11878; NID:9511819

R:Spengler, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.

J. Biol. Chem. 269, 11065-11072, 1994

A:Title: Structure, genomic organization, and expression of the human interleukin-8 receptor type B

A:Reference number: A53611; MUID:94209273; PMID:7512557

A:Accession: A53611

A:Molecule type: preliminary

A:Residues: 6-360 <SPR>

A:Cross-references: GB:M99412; GB:L19593

R:Murphy, P.M.; Tiffany, H.L.

Science 253, 1280-1283, 1991

A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor

A:Reference number: A39446; MUID:91368200; PMID:1891716

A:Accession: A39446

A:Status: preliminary

A:Molecule type: nucleic acid sequence not shown

A:Residues: 6-360 <MUR>

A:Cross-references: GB:M73969

C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, in C:Genetics:

A:Gene: GDB:IL8RB; IL8RA

A:Cross-references: GDB:127868; OMIM:146928

A:Map position: 2q35-2q35

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.4%; Score 534.5; DB 2; Length 360;
Best Local Similarity 33.2%; Pred. No. 2.2e-38;
Matches 120; Conservative 75; Mismatches 141; Indels 25; Gaps 8;

3 LEONOSTDYVEENMANGYDYSOYELI-----CIKEDVREFAKVELPFLIVIVIGLA 57

DB 6 MESDSFEDFPWKGEDLSNYSYSTLPFLILDAAPCEPSL-EINKYFVITIALVFLSL 64

QY 58 GNSMVAIYAYKKQRTYTDYIILNLAVALDLETPFMAVNAVGVNLKIMCKITSA 117

DB 65 GNSLVMALVILSRVGRSVTDVYLLNLADLLEFLTEPIMASKNGMIFCTFLCKVSL 124

QY 118 LYTLEFVSGMQLACISIDRYAV---TKVSQSGVSGPCWITCECVMAAILSLDPL 174

DB 125 LKEVNFYSGLILLACISIDRYAVIAHATRLTKRY--LVFICLSIMGSLILALPVL 182

QY 175 F---YVNDNARCIPIPRYIG---TSMKALIQMLEICIEFVPLIMGCVITARTL 227

DB 183 FRRRTYSSNVSPAC---EDMGNTATWMLRLRLPQSFYPLMLFECYFTLRTL 238

QY 228 MKMPTIKSRPLKVLTVIVIVITQVLYNIVKFCRAIDITSLTSCNMSKRMADIAIOV 287

DB 239 FKAHMGQKHRAKRVIFAVVLIFFLCWLPYNVVLADLTMRTOYIOETCERNHIDRALDA 298

QY 288 TSEIALFHSCLNDILYVENGASFKNYVMKAVKGSWRQ---RQSVFEPDSEGPTEP 344

DB 299 TETIGILHSCNLDPLIYAFIGQKFRHGLKILAIHGLISKDSLPRKDSRPSFVSSGHTST 358

QY 345 T 345

DB 359 T 359

RESULT 8

probable G protein-coupled receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C:Accession: J58186

R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord an

A:Reference number: J58186; MUID:94323113; PMID:8047298

A:Accession: J58186

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U04808; NID:92558635; PIDN:AA687093.1; PID:9439861

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 28.8%; Score 524; DB 2; Length 354;
Best Local Similarity 36.9%; Pred. No. 1.8e-37;
Matches 113; Conservative 51; Mismatches 128; Indels 14; Gaps 4;

QY 22 YDSQYELICKEDVREFAKVELPFLIVIVIGLAQNSMVAIYAYKKQRTYDYL 81

DB 13 FEYDDSAFACLGDIIVAGTIFLSIFSLVFTFGLVGNLVLALTNRSKRSSTIDYLL 72

QY 82 NLAVADLLETPFMAVNAVGVNLKIMCKITSAIYTNFVSGMQLACISIDRYAV 141

DB 73 NLALSDLFVATLPFPWTHYILSHGGLHNAKCKLTAFFIGFGIFIVISIDRLAI 132

QY 142 TKVPS-----QSGVGKPCWITCECVMAAILSLDPLVYVNDNARCIPIPRYLG 194

DB 133 VLAANSNNRTVOHG-----TISLGVMAAAILVASQPFMTFRKNK-ECLAGYPEVLQ 186

QY 195 SMKALIQMLEICIEFVPLIMGCVITARTLMKMNITISRLKVLTVIVITQV 254

DB 187 IWPVLRSSEVNIIGFVLPILMSCTYRIVRTLPSCNKKAKAIRLILVAVFLEWT 246

QY 255 PYNIVKFCRAIDITSLTSCNMSKRMADIAIOVTESTIALFHSCLNDPLLYVFGASFKNY 314

DB 247 PYNIVFLETLK-FYNFPSCGMKRLMALSVTEVAFHSCLNDPLIYAFAGEKRRRL 305

QY 315 MKVAKK 320

DB 306 RHLNKK 311

RESULT 9

JC4304

orphan G protein-coupled receptor - human

N:Alternate names: V28 protein

C:Species: Homo sapiens (man)

C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000

C:Accession: JC4304

R:Report, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.

Gene 163, 295-299, 1995

A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related t

A:Reference number: JC4304; MUID:96011651; PMID:7590284

A:Accession: JC4304

A:Molecule type: mRNA

A:Residues: 1-355 <RAP>

A:Cross-references: GB:U020350; NID:9665580; PIDN:AAA91783.1; PID:9665581

Db 303 ATGLPFRDRLRLRGSSSPGPPRRGCRPRRLS-----SCSAPTEHSL 350

RESULT 12

A53752

Interleukin-8 receptor (clone 5B1a) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: A53752

R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; Larosa, G.J.; Wilkinson, N.; Folco, E.; Navaroc J. Biol. Chem. 269, 12391-12394, 1994

A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isolate.

A:Reference number: A53752; MUID:94230294; PMID:8175642

A:Accession: A53752

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-358 <PRA>

A:Cross-references: GB:L24445; NID:9437661; PIDN:AAA31378.1; PID:9437662

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.1%; Score 511; DB 2; Length 358;

Best Local Similarity 32.3%; Pred. No. 2.3e-36;

Matches 116; Conservative 72; Mismatches 139; Indels 32; Gaps 8;

QY 10 DYEEENMGNTDYSOYELI-----CIKEDVREFAKFLPVLFTVYIGLA 57

Db 8 MYSTE--DFEG--DPSNTYSTDLPLLLDSAPCRSESLTNSVYLITYI-LVFLLSL 62

QY 58 GNSMVAIYAYKKQRTDVIILNLAVADLLFTLPFAVNAVHGVGKIMCKITSA 117

Db 63 GNSLVMVLVYRSSTGCVTDVILNLAIADLFTLPIAASKVHGTGTELCAYSL 122

QY 118 LYTINFSGQFLACISIDRYAV-----TKVPSQSGVGKPCWICFCVMAAILSTIPD 172

Db 123 VKENYFSYGLLACISVDRLAIHATRTMICKRLVK---FICLSMVGSLISLPI 178

QY 173 LVFTVMDNRCPIPEFRYLGTS---MKALIQMLEICGVVPELLMGVCFITATLWK 229

Db 179 LFRNALFPNNSPVCEMDGNSTAKRWVLRILPOTFGILPLVLMFCVYETLRLQ 238

QY 230 MPNIKSRPLKVLTVYIVETQLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAQVTE 289

Db 239 AHGQKRRARVIFAVVLLPLCMLPYNLVLTDLMTFRHVIGETCERRNDIDRALDNE 298

QY 290 SIALFHSCLPILYVPGAFKRYVWVAKKYSKMRQ---KQSVPEPPDSEGPTEPT 345

Db 299 ILGLFSLCLPILYAFIGOKFRYGLKLILAHGLISKEFLAKESRPSFVASSGNTSTP 357

RESULT 13

JO1231

Interleukin-8 receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999

C:Accession: JO1231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; Vandembos, T.; Price, V.; Lyman, S.; Gerard Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A:Title: Molecular characterization of the interleukin-8 receptor.

A:Reference number: JO1231; MUID:91378994; PMID:1896400

A:Accession: JO1231

A:Molecule type: DNA

A:Residues: 1-355 <BEC>

A:Cross-references: GB:M74240; NID:9165438; PIDN:AAA31375.1; PID:9165439

R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.

A:Reference number: A46483; MUID:92148149; PMID:1737938

A:Accession: A46483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-355 <LEB>

A:Cross-references: GB:M62873; NID:9165440; PIDN:AAA31376.1; PID:9165441

A:Experimental source: neutrophils

A:Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.6%; Score 501.5; DB 2; Length 355;

Best Local Similarity 33.1%; Pred. No. 1.5e-35;

Matches 107; Conservative 70; Mismatches 127; Indels 19; Gaps 6;

QY 12 YDEENMGNT-----YDSQYELCIKEDVREFAKFLPVLFTVYIGLAGNSMVAI 65

Db 14 WFERDEPAMATGMPVEKDY--PCLVVTQTLNKVVV--VYALVFLSLGNSLVMY 68

QY 66 YAYKKQRTDVIILNLAVADLLFTLPFAVNAVHGVGKIMCKITSAIYTLNFS 125

Db 69 ILKRSNRSTQDVIILNLAIADLFTLPFAVNAVHGVGKIMCKITSAIYTLNFS 128

QY 126 GMOFLACISIDRYAV-----TKVPSQSGVGKPCWICFCVMAAILSTIPOLVFTVNDNA 182

Db 129 GILLACISVDRLAIHATRTMICKRLVK---RHLVKFICIGIWLSTLSLPFLRQVSPN 186

QY 183 RCPIPRRYLG---ISMKALIQMLEICGVVPELLMGVCFITATLWKMPNITSPPL 239

Db 187 NSSPVCEYEDLGHNTAKRWVLRILPOTFGILPLVLMFCVYETLRLFOAHMGCKHRAM 246

QY 240 KVLTVVIVETQLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAQVTEIATLFSCLN 299

Db 247 RVFAVVLFLCMLPYNLVLTDLMTFRHVIGETCERRNDIDRALDTEILGLHSCLN 306

QY 300 PLIYVPMGASEKRYVWVAKKYG 322

Db 307 PLIYAFIGONFRNGLKMLARG 329

RESULT 14

A45747

neuropeptide Y/peptide YY receptor Y3 - human

N:Alternate names: fusin; HH89; leukocyte-derived seven-transmembrane receptor LESTR;

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999

C:Accession: A45747; A53103; I53006; I59444; I69203; S32761

R:Federapfel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-L Genomics 16, 707-712, 1993

A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a

A:Reference number: A45747; MUID:93315164; PMID:8325644

A:Accession: A45747

A:Molecule type: mRNA

A:Residues: 1-352 <FRD>

A:Cross-references: GB:M99293; NID:9292516; PIDN:AAA16617.1; PID:9292517

R:Roetscher, M.; Geisler, T.; O'Reilly, T.; Zwaehlen, R.; Bagdadijani, M.; Moser, B. J. Biol. Chem. 269, 232-237, 1994

A:Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is high

A:Reference number: A53103; MUID:94103215; PMID:8276799

A:Accession: A53103

A:Molecule type: mRNA

A:Residues: 1-352 <LOE>

A:Cross-references: EMBL:X71635; NID:9297099; PIDN:CAA50641.1; PID:9297100

R:Hezrog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.

DNA Cell Biol. 12, 465-471, 1993

A:Title: Molecular cloning, characterization, and localization of the human homolog t

A:Reference number: I53006; MUID:93319629; PMID:8329116

A:Accession: I53006

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <HER>

A:Cross-references: GB:I06797; NID:9414929; PIDN:AAA03209.1; PID:9414928

R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Regul. Pept. 47, 247-258, 1993

A:Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human hom

A:Reference number: I59444; MUID:94052833; PMID:8234509

A:Accession: I59444

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <RES>
A:Cross-references: GB:101639; NID:g189313; PIDN:AAAI6594.1; PID:g189314
R:Nomura, H., Nielsen, B.W., Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A>Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemokine
A:Reference number: 154751; MUID:94092629; PMID:7505609
A:Accession: 169203
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <RES>
A:Cross-references: GB:D10924; NID:g219868; PIDN:BAAO1722.1; PID:g219869
C:Genetics:
A:Gene: GDB:NPY3R; NPY3
A:Cross-references: GDB:230002; OMIM:162643
A:Map position: 2q21-2q21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Mon Mar 17 12:24:54 2003

us-09-686-020a-2.rag

Page 1

GenCore version 5.1.4-P5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:07:18 ; Search time 36 Seconds
(without alignments)
1295.492 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819
Sequence: 1 MAFQNSTDYTYEENMNG.....VEEPPFDEGPTPTSTFTSI 350

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A-Geneseq.101002.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-----------------------------|
| 1 | 1819 | 100.0 | 350 | 20 | AAV57290 Human BGCKr protei |
| 2 | 1819 | 100.0 | 350 | 20 | AAV17435 Human signal pepti |
| 3 | 1819 | 100.0 | 350 | 20 | AAW93169 Human HFTAO41 prot |
| 4 | 1819 | 100.0 | 350 | 21 | AAV94325 Human seven transm |
| 5 | 1819 | 100.0 | 350 | 22 | AAV80119 Human CCR11 protei |
| 6 | 1819 | 100.0 | 350 | 22 | AAV08994 Human G protein-co |
| 7 | 1819 | 100.0 | 350 | 22 | AAV67237 Amino acid sequenc |
| 8 | 1819 | 100.0 | 382 | 22 | AAV62389 Human chemokine re |
| 9 | 1814 | 99.7 | 349 | 20 | AAW93170 Human HFTAO41 prot |
| 10 | 1814 | 99.7 | 350 | 20 | AAV30125 A human seven-pass |

| | | | | | |
|----|------|------|-----|----|-----------------------------|
| 11 | 1810 | 99.5 | 350 | 21 | AAV71301 Human orphan G pro |
| 12 | 1810 | 99.5 | 350 | 21 | AAV02835 Human G protein co |
| 13 | 1808 | 99.4 | 350 | 20 | AAV37788 Human TSC7. Homo |
| 14 | 1728 | 95.0 | 333 | 20 | AAV57289 Human BGCKr partia |
| 15 | 1620 | 89.1 | 350 | 22 | AAV67238 Amino acid sequenc |
| 16 | 1591 | 87.5 | 350 | 20 | AAV57291 Mouse BGCKr protei |
| 17 | 1275 | 70.1 | 246 | 20 | AAV57292 Human BGCKr protei |
| 18 | 1257 | 69.1 | 242 | 22 | AAV57294 Human expressed po |
| 19 | 1212 | 66.6 | 263 | 20 | AAV30126 A seven-pass trans |
| 20 | 862 | 47.4 | 164 | 22 | AAV91162 Human orphan GPCR |
| 21 | 824 | 45.3 | 159 | 21 | AAV41786 Human ORFX ORF150 |
| 22 | 761 | 41.8 | 175 | 22 | AAV087280 Human ORFX ORF150 |
| 23 | 761 | 41.8 | 175 | 22 | AAV09976 Human expressed po |
| 24 | 761 | 41.8 | 175 | 22 | AAV10276 Human central nerv |
| 25 | 761 | 41.8 | 175 | 22 | AAV18161 Human ORFX ORF150 |
| 26 | 761 | 41.8 | 175 | 22 | AAV18161 Human ORFX ORF150 |
| 27 | 761 | 41.8 | 175 | 22 | AAV18165 Human ORFX ORF150 |
| 28 | 761 | 41.8 | 175 | 22 | AAV18165 Human ORFX ORF150 |
| 29 | 761 | 41.8 | 175 | 22 | AAV18165 Human ORFX ORF150 |
| 30 | 659 | 36.2 | 358 | 21 | AAV48724 Human 7TM receptor |
| 31 | 659 | 36.2 | 358 | 21 | AAV48724 Human 7TM receptor |
| 32 | 659 | 36.2 | 378 | 19 | AAV48724 Human 7TM receptor |
| 33 | 659 | 36.2 | 378 | 19 | AAV48724 Human 7TM receptor |
| 34 | 659 | 36.2 | 378 | 21 | AAV48724 Human 7TM receptor |
| 35 | 659 | 36.2 | 378 | 22 | AAV48724 Human 7TM receptor |
| 36 | 659 | 36.2 | 378 | 22 | AAV48724 Human 7TM receptor |
| 37 | 659 | 36.2 | 378 | 22 | AAV48724 Human 7TM receptor |
| 38 | 659 | 36.2 | 410 | 19 | AAV48724 Human 7TM receptor |
| 39 | 659 | 36.2 | 410 | 19 | AAV48724 Human 7TM receptor |
| 40 | 659 | 36.2 | 410 | 21 | AAV48724 Human 7TM receptor |
| 41 | 659 | 36.2 | 410 | 21 | AAV48724 Human 7TM receptor |
| 42 | 659 | 36.2 | 569 | 22 | AAV48724 Human 7TM receptor |
| 43 | 656 | 36.1 | 378 | 15 | AAV53744 Putative seven tra |
| 44 | 655 | 36.0 | 378 | 21 | AAV90663 Human mutant G pro |
| 45 | 653 | 35.9 | 378 | 21 | AAV90629 Human G protein-co |

ALIGNMENTS

| | | |
|----------|--|-------------------------------------|
| RESULT 1 | AAV57290 | AAV57290 standard; Protein: 350 AA. |
| ID | AAV57290 | |
| XX | AAV57290 | |
| AC | 05-JUN-2000 | (first entry) |
| XX | | |
| DE | Human BGCKr protein. | |
| XX | | |
| KW | Human BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis; | |
| KW | cell proliferation; anti-inflammatory; anti-angiogenic; anticancer; HIV; | |
| KW | anti-allergic; antiviral. | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO9952945-A2. | |
| XX | | |
| PD | 21-OCT-1999. | |
| XX | | |
| PF | 16-APR-1999; | 99NO-US08395. |
| XX | | |
| PR | 16-APR-1998; | 98US-0061753. |
| XX | | |
| PR | 16-APR-1999; | 99US-0061753. |
| XX | | |
| PA | (MILL-) MILLENIUM PHARM INC. | |
| PI | Gonzalo JA, Gutierrez-Ramos JC; | |
| XX | | |
| DR | WPI; 1999-620375/53. | |
| XX | N-PDB; AA290528. | |
| PT | New nucleic acid encoding human BGCKr receptor, used e.g. for | |

PT modulating inflammation and tumor growth
 PS Claim 8; Fig 2A-B; 123pp; English.
 XX

CC The invention relates to a human BGCR protein, a G-protein coupled
 CC receptor. The BGCR protein can be expressed by standard recombinant
 CC methodology. BGCR are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting; and exocytosis. The
 CC BGCR nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemotactic activity of leucocytes; angiogenesis; cell proliferation;
 CC tumor growth; allergic reactions and entry of human immune deficiency
 CC virus into cells; for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the full-length human BGCR protein.
 XX

Sequence 350 AA;

Query Match Best Local Similarity 100.0%; Score 1819; DB 20; Length 350;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M ALEONOSTDYEEENENGTYYDYSEYELICIKEDYREFAKYLPLVFLTYVIGLAGNS 60
 DB 1 M ALEONOSTDYEEENENGTYYDYSEYELICIKEDYREFAKYLPLVFLTYVIGLAGNS 60
 QY 61 MVAIAIYVYKRTKTDVYLLNLAVALDLLLFTLPFMAVNAVHGVNLCIKITTSALYT 120
 DB 61 MVAIAIYVYKRTKTDVYLLNLAVALDLLLFTLPFMAVNAVHGVNLCIKITTSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAAVTVKPSGSGVGPCKWITFCVMAAAILLSIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAAVTVKPSGSGVGPCKWITFCVMAAAILLSIPOLVFTVND 180
 QY 181 NARCIPFRYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNKISRPLK 240
 DB 181 NARCIPFRYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNKISRPLK 240
 QY 241 VLTIVYVYVYQLPYNYVKEFCRAIDIIYSLITSCNNSKRMDAIOVTSIALFHSCLNP 300
 DB 241 VLTIVYVYVYQLPYNYVKEFCRAIDIIYSLITSCNNSKRMDAIOVTSIALFHSCLNP 300
 QY 301 ILVFMGASFKNYVMYAKKYGSROROSVEEFPDSEGPTEPTSTFSI 350
 DB 301 ILVFMGASFKNYVMYAKKYGSROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 2

ID AAY17435 standard; Protein; 350 AA.
 AC AAY17435;
 XX

DT 29-JUL-1999 (first entry)
 XX

DE Human signal peptide-containing protein SP-16.
 XX

KW Human; signal peptide-containing protein; SP; cell proliferation;
 KW cancer; neuronal disorder; immune response; detection.
 XX

OS Homo sapiens.
 XX

PN WO9924463-A2.
 XX

PD 20-MAY-1999.
 XX

PF 04-NOV-1998; 98WC-US23578.
 XX

PR 07-NOV-1997; 97US-0966316.
 XX

PA (INCYT-) INCYTE PHARM INC.
 XX

PI Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;
 XX WPI: 1999-337694/28.
 DR N-PSDB: AAX61288.
 XX

PT cDNA clones encoding signal peptide-containing proteins
 PS Claim 1; Fig 1; 83pp; English.
 XX

CC The present sequence represents a human signal peptide-containing
 CC protein (SP), designated SP-16. SP proteins can be used to stimulate
 CC cell proliferation or to treat or prevent cancer. SP antagonists are
 CC also used to treat or prevent cancer, and also for treating or
 CC preventing neuronal disorders or immune responses. Polynucleotide
 CC sequences complementary to the SP-encoding nucleic acid molecules are useful
 CC for the detection of SP-encoding nucleic acid molecules in biological
 CC samples.
 XX

Sequence 350 AA;

Query Match Best Local Similarity 100.0%; Score 1819; DB 20; Length 350;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M ALEONOSTDYEEENENGTYYDYSEYELICIKEDYREFAKYLPLVFLTYVIGLAGNS 60
 DB 1 M ALEONOSTDYEEENENGTYYDYSEYELICIKEDYREFAKYLPLVFLTYVIGLAGNS 60
 QY 61 MVAIAIYVYKRTKTDVYLLNLAVALDLLLFTLPFMAVNAVHGVNLCIKITTSALYT 120
 DB 61 MVAIAIYVYKRTKTDVYLLNLAVALDLLLFTLPFMAVNAVHGVNLCIKITTSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAAVTVKPSGSGVGPCKWITFCVMAAAILLSIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAAVTVKPSGSGVGPCKWITFCVMAAAILLSIPOLVFTVND 180
 QY 181 NARCIPFRYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNKISRPLK 240
 DB 181 NARCIPFRYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLMKPNKISRPLK 240
 QY 241 VLTIVYVYVYQLPYNYVKEFCRAIDIIYSLITSCNNSKRMDAIOVTSIALFHSCLNP 300
 DB 241 VLTIVYVYVYQLPYNYVKEFCRAIDIIYSLITSCNNSKRMDAIOVTSIALFHSCLNP 300
 QY 301 ILVFMGASFKNYVMYAKKYGSROROSVEEFPDSEGPTEPTSTFSI 350
 DB 301 ILVFMGASFKNYVMYAKKYGSROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 3

ID AAW93169 standard; Protein; 350 AA.
 AC AAW93169;
 XX

DT 24-MAY-1999 (first entry)
 XX

DE Human HFI041 protein.
 XX

KW HFI041; G-coupled receptor; disease susceptibility; diagnosis; immunise;
 KW treatment; FIA041 protein; gene therapy; immune response; vaccine; HIV-2;
 KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
 KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
 KW benign prostatic hyperplasia; myocardial infarction; ulcer; asthma; schizophrenia;
 KW anxiety; manic depression; psychotic disorder; neurological disorder;
 KW dyslexia; Huntington's disease; Gilles de la Tourette's syndrome;
 KW linkage analysis; gene mapping; human.
 XX

OS Homo sapiens.
 XX

PN EP899332-A2.
 XX

Db 301 ILYVMGASFKNYMKVAKKYSWRROQSVEEFPDSEGGTEPTSTFSI 350

XX
DR
WPI: 1999-144803/13
PCDP: MAX22557.

Claim 1; page 22-23; 27pp; English

XX Claim 1, page 22-23, 27-31.

PS

CC This sequence represents a G-coupled receptor, HflA041 which is useful
CC for diagnosing susceptibility to diseases by detecting mutations in the
CC HflA041 gene, and can diagnose diseases associated with levels of HflA041 protein
CC imbalance by determining HflA041 polypeptide expression levels. Agonists
CC and antagonists of the protein can be used in treatment to activate
CC (agonist) or inhibit (antagonist) HflA041 activity, in addition to direct
CC administration of antisense sequences to prevent expression, or HflA041
CC polynucleotides to treat conditions associated with a lack of HflA041
CC protein. Gene therapy may also be used to affect endogenous HflA041
CC polypeptide expression. HflA041 antibodies are useful for inducing an
CC immune response to immunise and prevent disease, and for isolating
CC polypeptides or purifying the polypeptides by affinity chromatography.
CC HflA041 clones or purifying the polypeptides by affinity chromatography.
CC HflA041 polypeptides can be administered directly or as a vaccine to
CC inoculate against disease. Diseases diagnosed, prevented and treated
CC include bacterial, fungal, protozoan and viral infections, particularly
CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; myocardial infarction; ulcers;
CC resection; osteoporosis; angina pectoris; hypercalcaemia; urinary
CC asthma; allergies; benign prostatic hypertrophy; and psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, delirium, dementia, severe mental retardation and dyskinesias
CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
CC HflA041 polypeptide is also useful for mapping the gene to a chromosome,
CC allowing gene inheritance to be studied through linkage analysis.

| XX | sequence | 350 AA; | length 350; |
|----|----------|---------|-------------|
| SQ | | | |

| | | | | |
|-----------------------|--------------|---------------------|------------|--------------------|
| Query Match | 100.0%; | Score 1819; | DB | |
| Best Local Similarity | 100.0%; | Pred. No. 1.9e-195; | Indels | 0; |
| Matches 350; | Conservative | 0; | Mismatches | 0; |
| | | | | IndelTIVETGAGNS 60 |

| | | | |
|----|-----|--|-----|
| Qy | 1 | MALEQONOSTDYIYEENEMNGXVYXSOVELICIEDYERREKAFKELVEFLIT | 60 |
| Dd | 1 | MALEQONOSTDYIYEENEMNGITDIISOVELICIEDYERREKAFKELVEFLITVEFLI | 120 |
| Qy | 61 | MVAIIVAYYKKORTKTDVYILNLAVADLLIFLTPFAVNAVAGWGLKIMCKITSALT | 120 |
| Dd | 61 | MVAIIVAYYKKORTKTDVYILNLAVADLLIFLTPFAVNAVAGWGLKIMCKITSALT | 120 |
| Qy | 121 | LNFWSGMOFLACISIDRYAAVTKVPSQSGVSKPCWIIICFWMAAIIILSTPOLVEFYVND | 180 |
| Dd | 121 | LNFWSGMOFLACISIDRYAAVTKVPSQSGVSKPCWIIICFWMAAIIILSTPOLVEFYVND | 180 |
| Qy | 121 | LNFWSGMOFLACISIDRYAAVTKVPSQSGVSKPCWIIICFWMAAIIILSTPOLVEFYVND | 240 |
| Dd | 181 | NARCPIPEPRYLGTSMKALLOMEICIGVVPFELIMGVCYFTIARTLTKMKPNKISRPLK | 240 |
| Qy | 181 | NARCPIPEPRYLGTSMKALLOMEICIGVVPFELIMGVCYFTIARTLTKMKPNKISRPLK | 300 |
| Dd | 181 | NARCPIPEPRYLGTSMKALLOMEICIGVVPFELIMGVCYFTIARTLTKMKPNKISRPLK | 300 |
| Qy | 241 | VLTIVVAYIETOLPEYNIVAFRCRAIDIIYSILTSCMSKRMIDIAIOVETSIALFHSCLP | 300 |
| Dd | 241 | VLTIVVAYIETOLPEYNIVAFRCRAIDIIYSILTSCMSKRMIDIAIOVETSIALFHSCLP | 300 |
| Qy | 301 | ILVFWGSAFKNYVMKAKKGSWRROSGVEEPDSDGPEPIETSESI | 350 |

Db 301 ILYFMGASFKNYVMKVAKKYGSWIRROKOSVLELL...22--

| | RESULT 4 |
|-----------|-------------------------------------|
| AAV94325 | |
| ID | AAV94325 standard; Protein; 350 AA. |
| XX | |
| AAV94325; | |
| AC | |

11-AUG-2000 (first entry)

human seven transmembrane receptor VSHK-1.

DE human chorionic gonadotropin receptor; VSHK-1; signal transduction
XX human; seven transmembrane receptor; VSHK-1; signal transduction

XX KW HULLIAN, 2000

| | Homo sapiens: | Location/Qualifiers |
|----|---------------|---------------------|
| OS | | |
| XX | | |

| | | |
|----|---------------|---|
| FH | Key | 6.8 |
| FT | Modified-site | /note= "potential N-glycosylation site" |

| | | |
|---------------|--------|-------------------------|
| FT | /noce | |
| FT | 19..21 | "potential N-glycosylat |
| | (note= | |
| Modified-site | | |

| Domain | FT | FT | FT |
|----------------------|-------|-------|-------|
| Transmembrane_domain | 42.66 | 42.66 | 42.66 |

| Domain | Label | Transmembrane domain |
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| FT | 79..100 | |
| 2 | | |

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Domain
114..135
membrane domain
/label= transmembrane
FT

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| Domain | Label | Transmembrane |
|--------|----------|---------------|
| FT | 156..175 | |
| FI | | |
| Domain | | |

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Domain      /label=Transmembrane_...
FT          199..221

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Domain
Ff      Transmembrane domain
Ff      /label= Transmembrane domain
FT      241..262

```

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domain
FT      Transmembrane_domain
FT      /label=
FT      276..278

```

| Modified-site | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | 2101 | 2102 | 2103 | 2104 | 2105 | 2106 | 2107 | 2108 | 2109 | 2110 | 2111 | 2112 | 2113 | 2114 | 2115 | 2116 | 2117 | 2118 | 2119 | 2120 | 2121 | 2122 | 2123 | 2124 | 2125 | 2126 | 2127 | 2128 | 2129 | 2130 | 2131 | 2132 | 2133 | 2134 | 2135 | 2136 | 2137 | 2138 | 2139 | 2140 | 2141 | 2142 | 2143 | 2144 | 2145 | 2146 | 2147 | 2148 | 2149 | 2150 | 2151 | 2152 | 2153 | 2154 | 2155 | 2156 | 2157 | 2158 | 2159 | 2160 | 2161 | 2162 | 2163 | 2164 | 2165 | 2166 | 2167 | 2168 | 2169 | 2170 | 2171 | 2172 | 2173 | 2174 | 2175 | 2176 | 2177 | 2178 | 2179 | 2180 | 2181 | 2182 | 2183 | 2184 | 2185 | 2186 | 2187 | 2188 | 2189 | 2190 | 2191 | 2192 | 2193 | 2194 | 2195 | 2196 | 2197 | 2198 | 2199 | 2200 | 2201 | 2202 | 2203 | 2204 | 2205 | 2206 | 2207 | 2208 | 2209 | 2210 | 2211 | 2212 | 2213 | 2214 | 2215 | 2216 | 2217 | 2218 | 2219 | 2220 | 2221 | 2222 | 2223 | 2224 | 2225 | 2226 | 2227 | 2228 | 2229 | 2230 | 2231 | 2232 | 2233 | 2234 | 2235 | 2236 | 2237 | 2238 | 2239 | 2240 | 2241 | 2242 | 2243 | 2244 | 2245 | 2246 | 2247 | 2248 | 2249 | 2250 | 2251 | 2252 | 2253 | 2254 | 2255 | 2256 | 2257 | 2258 | 2259 | 2260 | 2261 | 2262 | 2263 | 2264 | 2265 | 2266 | 2267 | 2268 | 2269 | 2270 | 2271 | 2272 | 2273 | 2274 | 2275 | 2276 | 2277 | 2278 | 2279 | 2280 | 2281 | 2282 | 2283 | 2284 | 2285 | 2286 | 2287 | 2288 | 2289 | 2290 | 2291 | 2292 | 2293 | 2294 | 2295 | 2296 | 2297 | 2298 | 2299 | 2300 | 2301 | 2302 | 2303 | 2304 | 2305 | 2306 | 2307 | 2308 | 2309 | 2310 | 2311 | 2312 | 2313 | 2314 | 2315 | 2316 | 2317 | 2318 | 2319 | 2320 | 2321 | 2322 | 2323 | 2324 | 2325 | 2326 | 2327 | 2328 | 2329 | 2330 | 2331 | 2332 | 2333 | 2334 | 2335 | 2336 | 2337 | 2338 | 2339 | 2340 | 2341 | 2342 | 2343 | 2344 | 2345 | 2346 | 2347 | 2348 | 2349 | 2350 | 2351 | 2352 | 2353 | 2354 | 2355 | 2356 | 2357 | 2358 | 2359 | 2360 | 2361 | 2362 | 2363 | 2364 | 2365 | 2366 | 2367 | 2368 | 2369 | 2370 | 2371 | 2372 | 2373 | 2374 | 2375 | 2376 | 2377 | 2378 | 2379 | 2380 | 2381 | 2382 | 2383 | 2384 | 2385 | 2386 | 2387 | 2388 | 2389 | 2390 | 2391 | 2392 | 2393 | 2394 | 2395 | 2396 | 2397 | 2398 | 2399 | 2400 | 2401 | 2402 | 2403 | 2404 | 2405 | 2406 | 2407 |
|---------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
|---------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|

| Domain | 207-1031 |
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| FT | /label= Transmembrane-domain |
| FT | |

XX
XX
PN
WO200026369-A1.

11-MAY-2000.

03-NOV-1999: 99WO-US25848.

PF 03 NOV 1998: 98US-0107112.
XX 04 NOV 1998: 98US-0107112.

PR 04-NOV-1999; 99US-0114856.
PR 06-JAN-1999;

XX
PA (CHIR) CHIRON CORP.

XX Shymala V;
PI Khoja H,

XX
XX
WPJ: 2000-365618/31.

DR N-PSDB; AAY94325.

Novel polypeptide comprising a new amino acid and its encoding polynucleotide, useful for

XX 3. Fid 1: 79pp; English.

PS Claim 3, 1-19 =, 2-2
XX sequence is VSHK-1, a new sev

CC The present sequence of the membrane-spanning
CC receptor which contains seven membrane-spanning
CC regions and three intracellular amino acid loops

CC that are linked by unique restriction sites. The
CC sequence encoding VSHK-1 was isolated from
CC gene library 1 is predominantly found in

tissue, where VSHK-1 is present in a 1.3kb; a 2.0kb; and a 5.0kb fragment. The sequence corresponds to the 1.3kb; a 2.0kb; and a 5.0kb fragment.

encoding the present sequence of an alternative form may result from the use of an alternative form at nucleoside

transcription of a 3.0 kb influenza A virus promoter. VSHK-1 polynucleotides can inhibit transcription of other species.

CC 3.0-kb species and measure VSHK-1 mRNA. They
CC to detect and measure the level of VS
CC changes that modulate the level of VS

CC substances are...

CC sequence can be integrated into an expression vector for production of
CC VSHK-1 receptor polypeptides in host cells. The polypeptides can be used
CC to identify agents which modulate VSHK-1 receptor signal transduction
CC activity.
XX

SO Sequence 350 AA:

Query Match 100.0%; Score 1819; DB 21; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYEEENKNGTYDYSQYELICIKEDYREFAKFLPVLITVIGLAGNS 60
DB 1 MLEQNSTDYEEENKNGTYDYSQYELICIKEDYREFAKFLPVLITVIGLAGNS 60
QY 61 MVAIAYAYKKKORTKTDVYILNLAADLLFTLPMAVNAVHGVGKIMCKITTSALT 120
DB 61 MVAIAYAYKKKORTKTDVYILNLAADLLFTLPMAVNAVHGVGKIMCKITTSALT 120
QY 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWIIICFCVMAAILLSPOLVFTYVND 180
DB 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWIIICFCVMAAILLSPOLVFTYVND 180
QY 181 NARCIPIPRYIGTSMKALIOLEICIGFVPEFLIMGVCYFTARTLMKMPNIKISRPLK 240
DB 181 NARCIPIPRYIGTSMKALIOLEICIGFVPEFLIMGVCYFTARTLMKMPNIKISRPLK 240
QY 241 VLTAVIVIVITVQLPYNIVKFCRAIDITISLTSCNMSKRMIDIAIQVETSIALFHSCLNP 300
DB 241 VLTAVIVIVITVQLPYNIVKFCRAIDITISLTSCNMSKRMIDIAIQVETSIALFHSCLNP 300
QY 301 ILVPMGASFKNYVMKAKKYGSMRROSVEEPFDSGPEPTSTFSI 350
DB 301 ILVPMGASFKNYVMKAKKYGSMRROSVEEPFDSGPEPTSTFSI 350

RESULT 5
AAG80119
ID AAG80119 standard; Protein: 350 AA.

AC AAG80119;
XX

DT 17-JAN-2002 (first entry)
XX

DE Human CCR11 protein.
XX

KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW Inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW Chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antineoplastic; antiarthritic; immunosuppressive; dermatological;
KW

OS Homo sapiens.
XX

PN WO200172830-A2.
XX

PD 04-OCT-2001.
XX

PF 02-APR-2001: 2001WO-EP03708.
XX

PR 31-MAR-2000: 2000DE-1016013.
XX

PA (TPP-) IPF PHARM GMBH.
XX

PA (FORS/) FORSMANN U.
XX

PI Forssmann W, Adermann K, Heitland A, Spodsberg N;
XX

DR WPI; 2001-626256/72.
XX

PT Diagnostic agent containing two or more receptor-specific ligands,
XX

PT useful for detecting tumors, inflammation etc., also therapeutic use of
XX

XX ligand inhibitors

PS Disclosure; Page 11; 26pp; German.
XX

CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus)
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antineoplastic,
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR) which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention.
XX

SO Sequence 350 AA:

Query Match 100.0%; Score 1819; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYEEENKNGTYDYSQYELICIKEDYREFAKFLPVLITVIGLAGNS 60
DB 1 MLEQNSTDYEEENKNGTYDYSQYELICIKEDYREFAKFLPVLITVIGLAGNS 60
QY 61 MVAIAYAYKKKORTKTDVYILNLAADLLFTLPMAVNAVHGVGKIMCKITTSALT 120
DB 61 MVAIAYAYKKKORTKTDVYILNLAADLLFTLPMAVNAVHGVGKIMCKITTSALT 120
QY 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWIIICFCVMAAILLSPOLVFTYVND 180
DB 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWIIICFCVMAAILLSPOLVFTYVND 180
QY 181 NARCIPIPRYIGTSMKALIOLEICIGFVPEFLIMGVCYFTARTLMKMPNIKISRPLK 240
DB 181 NARCIPIPRYIGTSMKALIOLEICIGFVPEFLIMGVCYFTARTLMKMPNIKISRPLK 240
QY 241 VLTAVIVIVITVQLPYNIVKFCRAIDITISLTSCNMSKRMIDIAIQVETSIALFHSCLNP 300
DB 241 VLTAVIVIVITVQLPYNIVKFCRAIDITISLTSCNMSKRMIDIAIQVETSIALFHSCLNP 300
QY 301 ILVPMGASFKNYVMKAKKYGSMRROSVEEPFDSGPEPTSTFSI 350
DB 301 ILVPMGASFKNYVMKAKKYGSMRROSVEEPFDSGPEPTSTFSI 350

RESULT 6
AAU08994
ID AAU08994 standard; Protein: 350 AA.

AC AAU08994;
XX

DT 18-DEC-2001 (first entry)
XX

DE Human G protein-coupled receptor, GPCR, 2398.
XX

KW Human; GPCR; G protein-coupled receptor; 2398; cardiant;
KW antithrombotic; analgesic; cytoskeletal; angiogenic;
KW cardiovascular disorder; angiotensin-related disorder;
KW neural disorder; pain response disorder; inflammatory disorder;
KW atherosclerosis; angina pectoris; myocardial infarction;
KW ischaemic heart disease; sudden cardiac death; obesity;
KW hypertensive heart disease; diabetes; prostate cancer-related pain.
XX

OS Homo sapiens.
XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX
PN WO200164882-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06543.
XX
PR 29-FEB-2000; 2000US-186059P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA, Galvin KM, Slios-Santiago I;
XX
DR WPI; 2001-589866/66.
XX
DR N-PSDB; AAS14572.
XX
PT Novel G protein coupled receptors and nucleic acids encoding them, for
XX
PS identifying agents for the treatment of cardiac disorders
XX
PS Claim 9; Fig 9; 209pp; English.
XX
CC The invention relates to novel human G protein-coupled receptors (GPCR)
CC named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and
CC nucleic acids encoding them are useful for identifying agents for the
CC treatment of cardiovascular disorders, angiogenesis-related disorders,
CC neural disorders, pain response disorders and inflammatory disorders
CC e.g. atherosclerosis, angina pectoris and myocardial infarction,
CC ischemic heart disease, sudden cardiac death, hypertensive heart
CC disease, diabetes, prostate cancer-related pain, diabetes and obesity.
CC The present sequence represents GPCR 2398.
XX
SQ Sequence 350 AA:
XX
Query Match 100.0%; Score 1819; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MALEONOSTDYEEENEMNGTYDSOYELICKEDEYREFAVFLPVFLTIVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENEMNGTYDSOYELICKEDEYREFAVFLPVFLTIVFVIGLAGNS 60
XX
QY 61 MVAATYAYYKKORTDVTYILNLAVADLLFTLPFMAVNAVHGVGLKIMCKTTSALYT 120
DB 61 MVAATYAYYKKORTDVTYILNLAVADLLFTLPFMAVNAVHGVGLKIMCKTTSALYT 120
XX
QY 121 INFVSGMOFLACISIDRYVAATKVPSSGSGVGPWCWIIICFCVMAAILLSIPQLVFYTVND 180
DB 121 INFVSGMOFLACISIDRYVAATKVPSSGSGVGPWCWIIICFCVMAAILLSIPQLVFYTVND 180
XX
QY 181 NARCIPIPRYLGTSMAKALIQMLEICIGFVVPFLMGVCYFTARTLKMKNIKISRPK 240
DB 181 NARCIPIPRYLGTSMAKALIQMLEICIGFVVPFLMGVCYFTARTLKMKNIKISRPK 240
XX
QY 241 VLTAVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTIALFHSCCLNP 300
DB 241 VLTAVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTIALFHSCCLNP 300
XX
QY 301 ILVYEMGASRKNYVMKAKYKYSMBROROSVEEPFDSGPTPEPTSTFST 350
DB 301 ILVYEMGASRKNYVMKAKYKYSMBROROSVEEPFDSGPTPEPTSTFST 350
XX
RESULT 7
AAG67237 standard; protein; 350 AA.
ID AAG67237
XX
AC AAG67237;
XX
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of human chemokine receptor CCR11.
XX
KW Human; chemokine receptor; CCR11; G protein coupled receptor;

KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
KW asthma; angiogenesis; atherosclerosis vascular association disease;
KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
KW left ventricular diastolic dysfunction/migraine; preterm labour;
KW oesophageal spasm; ischemic stroke; subarachnoid haemorrhage;
KW myocardial infarction; congestive heart failure; endometriosi;
KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
XX
OS Homo sapiens.
XX
PN WO200166598-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US07073.
XX
PR 03-MAR-2000; 2000US-0186928.
XX
PR 03-MAR-2000; 2000US-0187231.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gray PM, Schmelckart VL, Epp A, Raport CJ, Chantry D, Steiner B;
XX
XX WPI; 2001-541918/60.
XX
DR N-PSDB; AAH77711.
XX
PT An isolated polynucleotide encoding the chemokine receptor CCR11,
PT useful for treating rheumatoid arthritis, inflammatory bowel disease,
PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's
PT phenomenon and migraine
XX
PS Claim 13; Page 96-97; 110pp; English.
XX
CC The present sequence represents the human chemokine receptor CCR11.
CC CCR11 is a member of the G protein coupled receptor family. A CCR11
CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
CC expression or biological activity, is useful for treating many
CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
CC bowel disease, and asthma. They are also useful for treating
CC angiogenesis, atherosclerosis vascular association diseases which may
CC include but are not limited to hypertension, angina pectoris, cardiac
CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
CC phenomenon, migraine, preterm labour, oesophageal spasm, ischemic
CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
CC heart failure, endometriosi, vasospasm, retinopathy, nephropathy, or
CC pulmonary vascular disease.
XX
SQ Sequence 350 AA:
XX
Query Match 100.0%; Score 1819; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MALEONOSTDYEEENEMNGTYDSOYELICKEDEYREFAVFLPVFLTIVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENEMNGTYDSOYELICKEDEYREFAVFLPVFLTIVFVIGLAGNS 60
XX
QY 61 MVAATYAYYKKORTDVTYILNLAVADLLFTLPFMAVNAVHGVGLKIMCKTTSALYT 120
DB 61 MVAATYAYYKKORTDVTYILNLAVADLLFTLPFMAVNAVHGVGLKIMCKTTSALYT 120
XX
QY 121 INFVSGMOFLACISIDRYVAATKVPSSGSGVGPWCWIIICFCVMAAILLSIPQLVFYTVND 180
DB 121 INFVSGMOFLACISIDRYVAATKVPSSGSGVGPWCWIIICFCVMAAILLSIPQLVFYTVND 180
XX
QY 181 NARCIPIPRYLGTSMAKALIQMLEICIGFVVPFLMGVCYFTARTLKMKNIKISRPK 240
DB 181 NARCIPIPRYLGTSMAKALIQMLEICIGFVVPFLMGVCYFTARTLKMKNIKISRPK 240
XX
QY 241 VLTAVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTIALFHSCCLNP 300
DB 241 VLTAVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTIALFHSCCLNP 300

OY 301 ILTVMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPTFSI 350
 DB 301 ILTVMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPTFSI 350

RESULT 8 AAB62389

ID AAB62389 standard; Protein; 382 AA.

AC AAB62389.

DT 29-JUN-2001 (first entry)

DE Human chemokine receptor CCX CKR polypeptide.

KW Chemokine receptor; CCX CKR; chemokine; ELC; SLIC; TECK; modulator;
 KW antiinflammatory; immunosuppressive; cytostatic; anti allergic; human;
 KW immunostimulant; gene therapy.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Misc-difference 351 /note= "encoded by TAA"

FT Misc-difference 353 /note= "encoded by TAA"

FT Misc-difference 365 /note= "encoded by TGA"

FT Misc-difference 371 /note= "encoded by TAA"

PN WO200127146-A2.

PD 19-APR-2001.

PF 10-OCT-2000; 2000WO-US28067.

PR 12-OCT-1999; 99US-0159015.

PR 13-OCT-1999; 99US-0159210.

PR 20-DEC-1999; 99US-0172979.

PR 28-DEC-1999; 99US-0173389.

PR 03-MAR-2000; 2000US-0186626.

PA (CHEM-) CHEMOCENTRIX INC.

PI Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;

DR WPI: 2001-281975/29.

DR N-PSDB: AAF57685.

PT Isolated or recombinant chemokine receptor (designated CCX CKR)

PT polypeptide (PI) or its fragment, useful for identifying CCX CKR

PT modulators which can be used in the treatment of inflammation, allergy,

PT an autoimmune disease or cancer -

PS Claim 4; Fig 1; 72pp; English.

XX The invention relates to an isolated or recombinant chemokine receptor

CC designated CCX CKR) polypeptide which binds to chemokines such as ELC,

CC SLIC or TECK. The CCX CKR polypeptide is useful for identifying CCX CKR

CC modulators. An agent that modulates the activity or expression of CCX CKR

CC in a cell or tissue in the mammal is useful in the treatment of a CCX CKR

CC mediated condition such as inflammation, allergy, an autoimmune disease,

CC graft rejection, cancer, an infectious disease or an immunosuppressive

CC disease. The present sequence represents the human CCX CKR polypeptide.

XX Sequence 382 AA:

Query Match 100.0%; Score 1819; DB 22; Length 382;

Best Local Similarity 100.0%; Pred. No. 2.2e-195;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MALEONOSTDYEEENMGNTYDYSOYELICIKEDVREFAKVLPLVFLTIVFVIGLAGNS 60

DB 1 MALEONOSTDYEEENMGNTYDYSOYELICIKEDVREFAKVLPLVFLTIVFVIGLAGNS 60
 OY 61 NVVAIYAYKKKORTKTDVYIINLAVADLLFTLPFMAVNAVHGVGKIMCKITTSALYT 120
 DB 61 NVVAIYAYKKKORTKTDVYIINLAVADLLFTLPFMAVNAVHGVGKIMCKITTSALYT 120
 OY 121 LNFVSGMOFLACISIDRVAATKVPSSGSGVGPWMICFCVMAAILLSTPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRVAATKVPSSGSGVGPWMICFCVMAAILLSTPOLVFTVND 180
 OY 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTRTLMKPNIKISPLK 240
 DB 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTRTLMKPNIKISPLK 240
 OY 241 VLLTVVIFYTYOLPYNIVKFCRAIDIIYSLITSCNMSKRDIAIOYTESIALFHSCLNP 300
 DB 241 VLLTVVIFYTYOLPYNIVKFCRAIDIIYSLITSCNMSKRDIAIOYTESIALFHSCLNP 300
 OY 301 ILTVMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPTFSI 350
 DB 301 ILTVMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPTFSI 350

RESULT 9

AAW93170 standard; Protein; 349 AA.

AAW93170;

DT 24-MAY-1999 (first entry)

XX Human HF1A04 protein.

DE HF1A04: G-coupled receptor; disease susceptibility; diagnosis; immunise;

KW treatment; F1A041 protein; gene therapy; immune response; vaccine; HIV-2;

KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;

KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;

KW hypotension; hypertension; urinary retention; osteoporosis; allergy;

KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;

KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;

KW anxiety; manic depression; delirium; dementia; severe mental retardation;

KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;

KW linkage analysis; gene mapping; human; ss.

OS Homo sapiens.

XX EP699332-A2.

PN 03-MAR-1999.

PD 17-FEB-1998; 98EP-0301170.

PF 27-OCT-1997; 97US-0962922.

PR 15-AUG-1997; 97US-0055895.

PA (SMK) SMITHKLINE BEECHAM CORP.

PI Ellis CE;

DR WPI: 1999-144803/13.

DR N-PSDB: AAX22558.

PT New G-coupled receptor (HF1A041) polypeptide and polynucleotide -

PT useful as diagnostic reagents and for prevention and treatment of

PT cancer, HIV infections and Parkinson's disease

PS Disclosure: Page 25-26; 27pp; English.

XX This sequence encodes a G-coupled receptor, HF1A041 which is useful for

CC diagnosing susceptibility to diseases by detecting mutations in the

CC HF1A041 gene, and can diagnose diseases associated with HF1A041 protein

CC imbalance by determining HF1A041 polypeptide expression levels. Agonists

CC and antagonists of the protein can be used in treatment to activate
CC (agonist) or inhibit (antagonist) Hf1a041 activity. In addition to direct
CC administration of antisense sequences to prevent expression, or Hf1a041
CC polynucleotides to treat conditions associated with a lack of Hf1a041
CC protein. Gene therapy may also be used to affect endogenous Hf1a041
CC polypeptide expression. Hf1a041 antibodies are useful for inducing an
CC immune response to immunize and prevent disease, and for isolating
CC Hf1a041 clones or purifying the polypeptides by affinity chromatography.
CC Hf1a041 polypeptides can be administered directly or as a vaccine to
CC inoculate against disease. Diseases diagnosed, prevented and treated
CC include bacterial, fungal, protozoan and viral infections, particularly
CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergies; benign prostatic hypertrophy; and psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, delirium, dementia, severe mental retardation and dyskinesias
CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
CC Hf1a041 polypeptide is also useful for mapping the gene to a chromosome,
CC allowing gene inheritance to be studied through linkage analysis.
XX

SO Sequence 349 AA;

Query Match 99.7%; Score 1814; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7e-195;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEQNSTDYEEENENGTYSQYELICIKEDVREFAKFLPVLTIVFVIGLAGNS 61
DB 1 ALEQNSTDYEEENENGTYSQYELICIKEDVREFAKFLPVLTIVFVIGLAGNS 60
QY 62 VVAIVAYKKQRTDVIILNLAVADLLFLTPFWAVNAVHGVLGKIMCKITSA 121
DB 61 VVAIVAYKKQRTDVIILNLAVADLLFLTPFWAVNAVHGVLGKIMCKITSA 120
QY 122 NFVSGMOFLACISIDRVAVATKVPSSGSGVKPCWIIICFCVMAAILLSTIPOLVFY 181
DB 121 NFVSGMOFLACISIDRVAVATKVPSSGSGVKPCWIIICFCVMAAILLSTIPOLVFY 180
QY 182 ARCIPIPRYLGTSMAKALQMLEICIGFVVPFLIMGVCFITARTLMKMPNIRPLK 241
DB 181 ARCIPIPRYLGTSMAKALQMLEICIGFVVPFLIMGVCFITARTLMKMPNIRPLK 240
QY 242 LLTVTVIVFYIYQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVETESIALFHSCLNP 301
DB 241 LLTVTVIVFYIYQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVETESIALFHSCLNP 300
QY 302 LLYVMGASFKNYVMKAKKYGSMRROSYVEEPPDESGTPTSTFSI 350
DB 301 LLYVMGASFKNYVMKAKKYGSMRROSYVEEPPDESGTPTSTFSI 349

RESULT 10

AA30125

ID AAY30125 standard; Protein: 350 AA.

XX AC AAY30125;

DT 14-OCT-1999 (first entry)

DE A human seven-pass transmembrane receptor protein.

KW Seven-pass transmembrane receptor; autoimmunity disease;

KM white blood cell dysfunction.

OS Homo sapiens.

PN WO933876-A1.

PD 08-JUL-1999.

PF 24-DEC-1998; 98WO-JP05886.

XX

PR 24-DEC-1997; 97JP-0354537.
XX (ASAH) ASAH KASEI KOGYO KK.
XX Ishimaru H, Koshio T, Ohno T;
PI WPI: 1999-493806/41.
DR N-PSDB: AAX86674.
XX New seven-pass transmembrane receptor protein useful for treating,
PT preventing or diagnosing autoimmune diseases
PS Claim 1: Page 101-103; 118pp; Japanese.
XX The present sequence represents a seven-pass transmembrane receptor
CC protein. The protein and its DNA can be used to screen substances
CC for the diagnosis, prevention and treatment of autoimmune diseases,
CC particularly those due to white blood cell dysfunction.
XX

SO Sequence 350 AA;

Query Match 99.7%; Score 1814; DB 20; Length 350;
Best Local Similarity 99.7%; Pred. No. 7e-195;
Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENENGTYSQYELICIKEDVREFAKFLPVLTIVFVIGLAGNS 60
DB 1 MALEQNSTDYEEENENGTYSQYELICIKEDVREFAKFLPVLTIVFVIGLAGNS 60
QY 61 MVAIVAYKKQRTDVIILNLAVADLLFLTPFWAVNAVHGVLGKIMCKITSA 120
DB 61 MVAIVAYKKQRTDVIILNLAVADLLFLTPFWAVNAVHGVLGKIMCKITSA 120
QY 121 INFVSGMOFLACISIDRVAVATKVPSSGSGVKPCWIIICFCVMAAILLSTIPOLVFY 180
DB 121 INFVSGMOFLACISIDRVAVATKVPSSGSGVKPCWIIICFCVMAAILLSTIPOLVFY 180
QY 181 NARCIPIPRYLGTSMAKALQMLEICIGFVVPFLIMGVCFITARTLMKMPNIRPLK 240
DB 181 NARCIPIPRYLGTSMAKALQMLEICIGFVVPFLIMGVCFITARTLMKMPNIRPLK 240
QY 241 VLLTVTVIVFYIYQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVETESIALFHSCLNP 300
DB 241 VLLTVTVIVFYIYQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVETESIALFHSCLNP 300
QY 301 LLYVMGASFKNYVMKAKKYGSMRROSYVEEPPDESGTPTSTFSI 350
DB 301 LLYVMGASFKNYVMKAKKYGSMRROSYVEEPPDESGTPTSTFSI 349

RESULT 11

AA71301

ID AAY71301 standard; Protein: 350 AA.

XX AC AAY71301;

DT 02-NOV-2000 (first entry)

DE Human orphan G protein-coupled receptor hppr1.

KW Human; orphan G protein-coupled receptor; GPCR; hppr1; drug screening;

KM transmembrane receptor; expressed sequence tag; EST; signal cascade.

OS Homo sapiens.

PN WO200031258-A2.

PD 02-JUN-2000.

PF 13-OCT-1999; 99WO-US23687.

PR 20-NOV-1998; 98US-0109213.

PR 16-FEB-1999; 99US-0120416.

PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123946.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0136567.
 PR 28-MAY-1999; 99US-0137127.
 PR 28-MAY-1999; 99US-0137131.
 PR 29-JUN-1999; 99US-0141448.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156634.
 PR 29-SEP-1999; 99US-0156653.
 PR 01-OCT-1999; 99US-0157280.
 PR 01-OCT-1999; 99US-0157281.
 PR 01-OCT-1999; 99US-0157282.
 PR 01-OCT-1999; 99US-0157293.
 PR 12-OCT-1999; 99US-0157294.
 PR 12-OCT-1999; 99US-0416760.
 PR 12-OCT-1999; 99US-0417044.

(AREN-) ARENA PHARM INC.

PI Chen R, Dang HT, Liao CW, Lin I;

WPI; 2000-40068/34.

DR N-PSDB; AAD01128.

PT Novel human orphan G protein-coupled receptors and the encoding cDNAs
 for use in the identification of G protein-coupled receptor agonists -

Claim 42; Page 69-70; 102pp; English.

CC The present amino acid sequence is the hpprl, an endogenous human
 CC orphan G protein-coupled receptor (GPCR), expressed in the pituitary
 CC gland, heart, salivary gland, small intestine and testis. The hpprl cDNA
 CC was identified using EST (expressed sequence tag) AA35504 and 238667 as
 CC a probe. The orphan GPCR of the invention, like all GPCRs has seven
 CC transmembrane alpha helices with an extracellular N-terminus and an
 CC intracellular C-terminus. However, no endogenous ligands has yet been
 CC identified for the proteins of the invention. The orphan GPCRs may be
 CC used in the identification of their endogenous ligands, and to screen
 CC potential GPCR agonists and antagonists for use as pharmaceutical agents.
 CC The proteins may also be used in the study of GPCR-mediated signalling
 CC cascades, and to elucidate their precise role in normal and diseased
 CC human conditions. Nucleic acid encoding human orphan GPCRs may be used
 CC for tissue localisation expression analysis to provide information about
 CC their function in healthy and pathological states.

SQ Sequence 350 AA:

Query Match 99.5%; Score 1810; DB 21; Length 350;

Best Local Similarity 99.4%; Pred. No. 2e-194; Mismatches 2; Indels 0; Gaps 0;

DB 1 MALEONOSTDYEEENEMNGTIDYSEYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60
 1 MALEONOSTDYEEENEMNGTIDYSEYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60

OY 61 MVAIVAYVYKRRKRTDVYILNLAVALDLLLFLPFAVAVAAGVGLKMKCTITSLATY 120
 61 MVAIVAYVYKRRKRTDVYILNLAVALDLLLFLPFAVAVAAGVGLKMKCTITSLATY 120

DB 61 MVAIVAYVYKRRKRTDVYILNLAVALDLLLFLPFAVAVAAGVGLKMKCTITSLATY 120
 61 MVAIVAYVYKRRKRTDVYILNLAVALDLLLFLPFAVAVAAGVGLKMKCTITSLATY 120

OY 121 LNFVSGMFLACISIDRYAVATKVPSSGVKPCWIIICFCVMAAILLSIPOLVFTVND 180
 121 LNFVSGMFLACISIDRYAVATKVPSSGVKPCWIIICFCVMAAILLSIPOLVFTVND 180

DB 121 LNFVSGMFLACISIDRYAVATKVPSSGVKPCWIIICFCVMAAILLSIPOLVFTVND 180
 121 LNFVSGMFLACISIDRYAVATKVPSSGVKPCWIIICFCVMAAILLSIPOLVFTVND 180

OY 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKPNIKISRPK 240
 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKPNIKISRPK 240

DB 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKPNIKISRPK 240
 181 NARCIPIFPRYLGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKPNIKISRPK 240

OY 241 VLVTVIVFVITQLPYIVAFRCRAIDITISLTSCNMSKMDIAIOVTESIALFHSCLNP 300
 241 VLVTVIVFVITQLPYIVAFRCRAIDITISLTSCNMSKMDIAIOVTESIALFHSCLNP 300

DB 241 VLVTVIVFVITQLPYIVAFRCRAIDITISLTSCNMSKMDIAIOVTESIALFHSCLNP 300
 241 VLVTVIVFVITQLPYIVAFRCRAIDITISLTSCNMSKMDIAIOVTESIALFHSCLNP 300

OY 301 ILYVFMGASFKNYVMKVKKYSMROROSVEEPFDESGTEPTSTSI 350
 301 ILYVFMGASFKNYVMKVKKYSMROROSVEEPFDESGTEPTSTSI 350

RESULT 12
 AAB02835
 ID AAB02835 standard; Protein: 350 AA.

XX AAB02835;

DT 22-AUG-2000 (first entry)

DE Human G protein coupled receptor hpprl protein seq ID NO:24.

KW Human; G protein coupled receptor; GPCR; transmembrane receptor;

KW Identification; agonist; screening; therapeutic; pharmaceutical;

KW mutant.

OS Homo sapiens.

PN WO200022131-A2.

PD 20-APR-2000.

PF 13-OCT-1999; 99WO-US24065.

PR 13-OCT-1998; 98US-01170496.

PR 12-NOV-1998; 98US-0108029.

PR 27-NOV-1998; 98US-0109213.

PR 16-FEB-1999; 98US-0110060.

PR 26-FEB-1999; 98US-0120416.

PR 12-MAR-1999; 98US-0121852.

PR 12-MAR-1999; 98US-0123944.

PR 12-MAR-1999; 98US-0123945.

PR 12-MAR-1999; 98US-0123946.

PR 12-MAR-1999; 98US-0123948.

PR 12-MAR-1999; 98US-0123949.

PR 12-MAR-1999; 98US-0123951.

PR 28-MAY-1999; 98US-0136436.

PR 28-MAY-1999; 98US-0136437.

PR 28-MAY-1999; 98US-0136439.

PR 28-MAY-1999; 98US-0137127.

PR 28-MAY-1999; 98US-0137131.

PR 30-JUN-1999; 98US-0141448.

PR 27-AUG-1999; 98US-0151114.

PR 03-SEP-1999; 98US-0152524.

PR 29-SEP-1999; 98US-0156633.

PR 29-SEP-1999; 98US-0156655.

PR 29-SEP-1999; 98US-0156634.

(AREN-) ARENA PHARM INC.

PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

Gore M, Liao CW, Lin I, Lowitz K, White C;

WPI; 2000-317986/27.

DR N-PSDB; AAA46029.

PT Non-endogenous, human G protein-coupled receptors for screening

receptor, inverse or partial agonists useful as therapeutic agents -

Example 1; Page 99-100; 187pp; English.

CC The present invention describes transmembrane receptors, preferably

CC human G protein coupled receptors (GPCR), for which the endogenous

CC ligand is unknown (orphan GPCR receptors). More specifically the present

CC invention relates to non-endogenous, constitutively activated versions

CC of a human GPCR. These non-endogenous human GPCRs can be useful for

CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
 CC the exemplification of the present invention.

XX Sequence 350 AA;

Query Match 99.5%; Score 1810; DB 21; Length 350;
 Best Local Similarity 99.4%; Pred. No. 2e-194;
 Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREFAKVFPLVLTIVVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREFAKVFPLVLTIVVIGLAGNS 60
 QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVNAHGWVLGIMCKITSALT 120
 DB 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVNAHGWVLGIMCKITSALT 120
 QY 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPOLVFYVND 180
 DB 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPOLVFYVND 180
 QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKPNKISRPLK 240
 DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKPNKISRPLK 240
 QY 241 VLTAVIYVFTQLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIQTESIATLFSCLNP 300
 DB 241 VLTAVIYVFTQLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIQTESIATLFSCLNP 300
 QY 301 ILVYFMGASFKNYVMKAKKYGSMRROSVSEFPDSEGPTEPTSTFSI 350
 DB 301 ILVYFMGASFKNYVMKAKKYGSMRROSVSEFPDSEGPTEPTSTFSI 350

RESULT 13

AAB37788 standard; Protein: 350 AA.

XX AAB37788;

DT 23-FEB-2001 (first entry)

DE Human TSC7.

XX Human: TSC; tuberous sclerosis complex; cytosstatic; antimicrobial;
 KW osteopathic; antiulcer; antistimatic; antiallergic; neuroprotective;
 KW cardiant; hypotensive; hypertensive; nootropic; anticonvulsant;
 KW analgesic; tranquilizer; immunosuppressive; antiinflammatory;
 KW gene therapy; TSC7; infection; cancer; autoimmune disorder;
 KW Parkinson's disease; osteoporosis; neurological disorder.

OS Homo sapiens.

PN WO200064941-A2.

PD 02-NOV-2000.

PE 21-APR-2000; 2000MO-US10979.

PR 23-APR-1999; 9905-0130817.

PR 20-APR-2000; 2000US-0556002.

PA (CURA-) CURAGEN CORP.

PI Gould-Rothberg BE;

WI; 2000-679670/66.

DR N-PSDB: AAC68722.

PT Novel nucleic acid encoding G-protein coupled receptor for diagnosis
 and treatment of conditions associated with disorder in a G-protein

PT mediated pathway such as cancer, neurological disorders and infections
 PS Claim 12; Page 8; 132pp; English.

CC The present sequence is human tuberous sclerosis complex 7 (TSC7).
 CC TSC7 polynucleotides and polypeptides are useful for determining the
 CC presence or predisposition to a disease associated with altered levels of
 CC TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the
 CC polypeptide are useful for treating or preventing pathological conditions
 CC associated with the disorder in a G-protein mediated pathway. They are
 CC useful for diagnosing a hyperproliferative condition such as a neoplasm
 CC or dermatological condition. TSC7 nucleic acids and polypeptides are
 CC useful in the treatment of microbial infections, pain, cancer, anorexia,
 CC asthma, autoimmune disorders, Parkinson's disease, acute heart failure,
 CC hypo/hypertension, osteoporosis, multiple sclerosis, angina pectoris,
 CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy
 CC and psychotic and neurological disorders, including schizophrenia,
 CC dementia, severe mental retardation and dyskinesias, such as
 CC Huntington's disease and/or other pathologies and disorders. TSC7
 CC polypeptides are also useful as immunogens to produce antibodies and as
 CC vaccines.

XX Sequence 350 AA;

Query Match 99.4%; Score 1808; DB 21; Length 350;
 Best Local Similarity 99.4%; Pred. No. 3.3e-194;
 Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREFAKVFPLVLTIVVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREFAKVFPLVLTIVVIGLAGNS 60
 QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVNAHGWVLGIMCKITSALT 120
 DB 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVNAHGWVLGIMCKITSALT 120
 QY 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPOLVFYVND 180
 DB 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPOLVFYVND 180
 QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKPNKISRPLK 240
 DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKPNKISRPLK 240
 QY 241 VLTAVIYVFTQLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIQTESIATLFSCLNP 300
 DB 241 VLTAVIYVFTQLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIQTESIATLFSCLNP 300
 QY 301 ILVYFMGASFKNYVMKAKKYGSMRROSVSEFPDSEGPTEPTSTFSI 350
 DB 301 ILVYFMGASFKNYVMKAKKYGSMRROSVSEFPDSEGPTEPTSTFSI 350

RESULT 14

AAY57289 standard; Protein: 333 AA.

XX AAY57289;

DT 05-JUN-2000 (first entry)

DE Human BGCR partial amino acid sequence.

XX BGCR protein: G-protein coupled receptor; human; chemokine; exocytosis;
 KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
 KW anti-allergic; antiviral.

OS Homo sapiens.

PN WO9952945-A2.

PD 21-OCT-1999.

XX 16-APR-1999; 99MO-US08395.
 XX 16-APR-1998; 98US-0061753.
 PR 16-APR-1999; 99US-0061753.
 XX (MILL-) MILLENIUM PHARM INC.
 PA
 XX Gonzalez JA, Gutierrez-Ramos JC;
 PI
 XX MPI: 1999-620375/53.
 DR N-PSDB: AA290527.
 XX
 PT New nucleic acid encoding human BGCR receptor, used e.g. for
 PT modulating inflammation and tumor growth
 XX
 XX Claim 1; Fig 1A-B; 123pp; English.
 XX
 CC The invention relates to a human BGCR protein, a G-protein coupled
 CC receptor. The BGCR protein can be expressed by standard recombinant
 CC methodology. BGCR are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BGCR nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemottractant activity of leucocytes; angiogenesis; cell proliferation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the sequence of a partial human BGCR protein.
 XX
 XX Sequence 333 AA;

Query Match 95.0%; Score 1728; DB 20; Length 333;
 Best Local Similarity 100.0%; Pred. No. 3e-185;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 MNGTYDSQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNSMVAIVAYKKQRTKD
 DB 1 MNGTYDSQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNSMVAIVAYKKQRTKD 60
 QY 78 VYIINLAADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYTNFSGMOFLACISIDR 137
 DB 61 VYIINLAADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYTNFSGMOFLACISIDR 120
 QY 138 YVAATKVPSSQSGVGRPCWIIICFCYMAAIIISIPQVLYFYVNDNARCIPIPRYLGTSMK 197
 DB 121 YVAATKVPSSQSGVGRPCWIIICFCYMAAIIISIPQVLYFYVNDNARCIPIPRYLGTSMK 180
 QY 198 ALIOMLEICIGFVVPFLIMGVCFYTTARTLMKMPNIRKISRPKVLTVVIVITQLPYN 257
 DB 181 ALIOMLEICIGFVVPFLIMGVCFYTTARTLMKMPNIRKISRPKVLTVVIVITQLPYN 240
 QY 258 IVKCRADIIYSLITSCNMSKRMIDIAIOVTESTALFHSCNPLIYVFMGASFNKYMKV 317
 DB 241 IVKCRADIIYSLITSCNMSKRMIDIAIOVTESTALFHSCNPLIYVFMGASFNKYMKV 300
 QY 318 AKKYGSMRQROSVYEEFPDESGTEPTSTFSI 350
 DB 301 AKKYGSMRQROSVYEEFPDESGTEPTSTFSI 333

RESULT 15
 AAG67238
 ID AAG67238 standard; Protein: 350 AA.
 XX
 AC AAG67238;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of bovine chemokine receptor CCR1.
 XX
 KW Human; chemokine receptor; CCR1; G protein coupled receptor;

KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
 KW asthma; angiogenesis; atherosclerosis vascular association disease;
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
 KW left ventricular diastolic dysfunction; migraine; preterm labour;
 KW oesophageal spasm; ischemic stroke; subarachnoid haemorrhage;
 KW myocardial infarction; congestive heart failure; endometritis;
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
 XX
 OS Bos sp.
 XX
 PN WO200166598-A2.
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US07073.
 XX
 PR 03-MAR-2000; 2000US-0186928.
 PR 03-MAR-2000; 2000US-0187231.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
 DR MPI: 2001-541918/60.
 DR N-PSDB: AAH77712.

XX
 PS Example 1; Page 99-100; 110pp; English.
 XX
 CC The present sequence represents the bovine chemokine receptor CCR1.
 CC CCR1 is a member of the G protein coupled receptor family. A CCR1
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR1
 CC expression or biological activity, is useful for treating many
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
 CC bowel disease, and asthma. They are also useful for treating
 CC angiogenesis, atherosclerosis vascular association diseases which may
 CC include but are not limited to hypertension, angina pectoris, cardiac
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischemic
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
 CC heart failure, endometritis, vasospasm, retinopathy, nephropathy, or
 CC pulmonary vascular disease.
 CC
 CC Sequence 350 AA;

Query Match 89.1%; Score 1620; DB 22; Length 350;
 Best Local Similarity 86.0%; Pred. No. 4.2e-173;
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEQNSIDYEEENMGTYDSQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEYQSDTYEEENMGTYDSQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAIVAYKKQRTKDYIILNLAADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYT 120
 DB 61 TVVAIAAYKKRRTKDYIILNLAADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYT 120
 QY 121 LNEVSGMOFLACISIDRYAATKVPSSQSGVGRPCWIIICFCYMAAIIISIPQVLYFYVND 180
 DB 121 VNEVSGMOFLACISIDRYAATKVPSSQSGVGRPCWIIICFCYMAAIIISIPQVLYFYVNH 180
 QY 181 NARCIPIPRYLGTSMKALIOMLEICIGFVVPFLIMGVCFYTTARTLMKMPNIRKISRPK 240
 DB 181 KARCVPIPRYLGTSMKASIQLEICIGFVVPFLIMGVCFYTTARTLMKMPNIRKISRPK 240
 QY 241 VLTFTVIVIVITQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIOVTESTALFHSCNLP 300
 DB 241 VLTFTVIVIVITQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIOVTESTALFHSCNLP 300

OY 301 ILYVPMGASFKNYVMKVAKKYGSWROROSVEEPPDSECPTEPTSTFSI 350
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
DB 301 VLYVPMGTSPFNKNTMKVAKKYGSMWRORONVEIPESEDATEPTSTFSI 350

Search completed: March 14, 2003, 16:11:25
Job time : 38 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:09:57 ; Search time 15 seconds
(without alignments)
686.535 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEQNGSTDTYYEENMNG.....VEEFPDSDGPTPTSTFST 350

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1819 | 100.0 | 350 | 2 | US-08-966-316-16 |
| 2 | 1620 | 89.1 | 350 | 2 | US-08-966-316-18 |
| 3 | 659 | 36.2 | 358 | 1 | US-08-153-848-19 |
| 4 | 659 | 36.2 | 358 | 3 | US-09-299-843A-19 |
| 5 | 659 | 36.2 | 358 | 4 | US-09-088-337B-19 |
| 6 | 659 | 36.2 | 358 | 5 | PCT-US93-11153-19 |
| 7 | 659 | 36.2 | 378 | 1 | US-08-153-848-15 |
| 8 | 659 | 36.2 | 378 | 3 | US-09-299-843A-15 |
| 9 | 659 | 36.2 | 378 | 4 | US-09-251-545-1 |
| 10 | 659 | 36.2 | 378 | 4 | US-09-088-337B-15 |
| 11 | 659 | 36.2 | 378 | 5 | PCT-US93-11153-15 |
| 12 | 659 | 36.2 | 410 | 1 | US-08-153-848-7 |
| 13 | 659 | 36.2 | 410 | 3 | US-09-299-843A-7 |
| 14 | 659 | 36.2 | 410 | 4 | US-09-088-337B-7 |
| 15 | 659 | 36.2 | 410 | 5 | PCT-US93-11153-7 |
| 16 | 650 | 35.7 | 378 | 4 | US-09-299-843A-66 |
| 17 | 650 | 35.7 | 378 | 4 | US-09-088-337B-66 |
| 18 | 643 | 35.3 | 378 | 1 | US-08-383-750-2 |
| 19 | 643 | 35.3 | 378 | 1 | US-08-383-751A-2 |
| 20 | 643 | 35.3 | 378 | 3 | US-08-352-678-2 |
| 21 | 643 | 35.3 | 378 | 4 | US-09-045-583-49 |
| 22 | 643 | 35.3 | 378 | 4 | US-09-534-185-49 |
| 23 | 643 | 35.3 | 378 | 5 | PCT-US93-09636-2 |
| 24 | 637 | 35.0 | 357 | 4 | US-09-266-464-2 |
| 25 | 635.5 | 34.9 | 359 | 1 | US-08-153-848-24 |
| 26 | 635.5 | 34.9 | 359 | 3 | US-09-299-843A-24 |
| 27 | 635.5 | 34.9 | 359 | 4 | US-09-088-337B-24 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 635.5 | 34.9 | 359 | 5 | PCT-US93-11153-24 | Sequence 24, Appl |
| 29 | 606.5 | 33.3 | 361 | 2 | US-08-902-294-2 | Sequence 2, Appl |
| 30 | 606.5 | 33.3 | 361 | 3 | US-09-178-637-2 | Sequence 2, Appl |
| 31 | 583 | 32.1 | 374 | 4 | US-09-045-583-48 | Sequence 48, Appl |
| 32 | 583 | 32.1 | 374 | 4 | US-09-534-185-48 | Sequence 48, Appl |
| 33 | 581 | 31.9 | 342 | 4 | US-09-116-498-4 | Sequence 6, Appl |
| 34 | 569 | 31.3 | 342 | 4 | US-09-116-498-6 | Sequence 2, Appl |
| 35 | 560 | 30.8 | 342 | 2 | US-08-742-011-2 | Sequence 5, Appl |
| 36 | 560 | 30.8 | 342 | 4 | US-09-116-498-2 | Sequence 2, Appl |
| 37 | 560 | 30.8 | 342 | 4 | US-09-449-437A-2 | Sequence 2, Appl |
| 38 | 560 | 30.8 | 342 | 4 | US-09-517-605-9 | Sequence 9, Appl |
| 39 | 537.5 | 29.5 | 360 | 4 | US-08-875-573-20 | Sequence 20, Appl |
| 40 | 537.5 | 29.5 | 360 | 4 | US-09-232-878-2 | Sequence 2, Appl |
| 41 | 537.5 | 29.5 | 360 | 4 | US-09-045-583-55 | Sequence 55, Appl |
| 42 | 537.5 | 29.5 | 360 | 4 | US-09-534-185-55 | Sequence 55, Appl |
| 43 | 534.5 | 29.4 | 355 | 1 | US-07-759-568-1 | Sequence 1, Appl |
| 44 | 534.5 | 29.4 | 355 | 1 | US-08-450-393A-8 | Sequence 8, Appl |
| 45 | 534.5 | 29.4 | 355 | 1 | | |

ALIGNMENTS

RESULT 1
US-08-966-316-16
Sequence 16, Application US/08966316
Patent No. 593245
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murthy, Lynn E.
APPLICANT: Mathur, Preetee
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSNCT11
CLONE: 2547002
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.7e-147;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENGTYSQYELICIKEDVREFAKVLPVLTIVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENENGTYSQYELICIKEDVREFAKVLPVLTIVFVIGLAGNS 60
QY 61 MVAATAYAYKKORFTDYIILNLAVALDLFLTPMAVANAHVGLGIMCKITSALYT 120
DB 61 MVAATAYAYKKORFTDYIILNLAVALDLFLTPMAVANAHVGLGIMCKITSALYT 120
QY 121 LNFVSGMOFLACISIDRYAAVTKVPSSGVGRPCWIIICFCVMAAIIISIPOLVFYVND 180
DB 121 LNFVSGMOFLACISIDRYAAVTKVPSSGVGRPCWIIICFCVMAAIIISIPOLVFYVND 180
QY 181 NARCPITPRYLGTSMKALIQMLEICIGFVVPPLMGVCYFTARTLMKMPNIKISRLK 240
DB 181 NARCPITPRYLGTSMKALIQMLEICIGFVVPPLMGVCYFTARTLMKMPNIKISRLK 240
QY 241 VLTFTVIVFIVTOLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIOVTESTIALFHSCLP 300
DB 241 VLTFTVIVFIVTOLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIOVTESTIALFHSCLP 300
QY 301 ILVYFMGASFKNYKVMKAKKYSWRROQSVVEEPFSEGPTEPTSTFSI 350
DB 301 ILVYFMGASFKNYKVMKAKKYSWRROQSVVEEPFSEGPTEPTSTFSI 350

RESULT 2

US-08-966-316-18
Sequence 18, Application US/08966316
Patent No. 5932445

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa E.
APPLICANT: Murthy, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 399711
US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.4e-130;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENGTYSQYELICIKEDVREFAKVLPVLTIVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENENGTYSQYELICIKEDVREFAKVLPVLTIVFVIGLAGNS 60
QY 61 MVAATAYAYKKORFTDYIILNLAVALDLFLTPMAVANAHVGLGIMCKITSALYT 120
DB 61 MVAATAYAYKKORFTDYIILNLAVALDLFLTPMAVANAHVGLGIMCKITSALYT 120
QY 121 LNFVSGMOFLACISIDRYAAVTKVPSSGVGRPCWIIICFCVMAAIIISIPOLVFYVND 180
DB 121 LNFVSGMOFLACISIDRYAAVTKVPSSGVGRPCWIIICFCVMAAIIISIPOLVFYVND 180
QY 181 NARCPITPRYLGTSMKALIQMLEICIGFVVPPLMGVCYFTARTLMKMPNIKISRLK 240
DB 181 NARCPITPRYLGTSMKALIQMLEICIGFVVPPLMGVCYFTARTLMKMPNIKISRLK 240
QY 241 VLTFTVIVFIVTOLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIOVTESTIALFHSCLP 300
DB 241 VLTFTVIVFIVTOLPYNIYKFCRAIDIIYSLITSCNMSKRMIDIAIOVTESTIALFHSCLP 300
QY 301 ILVYFMGASFKNYKVMKAKKYSWRROQSVVEEPFSEGPTEPTSTFSI 350
DB 301 ILVYFMGASFKNYKVMKAKKYSWRROQSVVEEPFSEGPTEPTSTFSI 350

RESULT 3

US-08-153-848-19
Sequence 19, Application US/08153848
Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-19

Query Match 36.2%; Score 659; DB 1; Length 358;
Best Local Similarity 38.7%; Pred. No. 9,7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

1 MALEONOSTDYEEENMGTYDYOYELICEDVREFAKVLPVFLTVFVIGLAGNS 60
1 VCLQDEVDYDIGNT---TVDTLFEISCKKDVNFAMFLPIMYSIICFVGLGNG 57
61 MVAIYAYKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVGLKIMCKITSAIYT 120
58 LVVLYIYFKRKTMDTYLNLAVADILFTLPFAVNAVHGVGLKIMCKITSAIYT 117
121 LNFVSGMQLACISIDRYAVATKVP---QSGVGKPCWIIICVMAAILSIPLVFEY 176
118 MSFSGMQLLICTIDRYAIVQAVSAHRRARVLLISKSCVGIWILATVLSIPELLXS 177
177 TVNDNA-----RCIPFPRLGTSMKALIQMLEICIGFVPLMGVCYFITTARTLMKMP 231
178 DLQSSSEQAMRCSLITEH---VEAFITIQVQVGMVIGFLPLAMSFVYIITRLLOAR 234
232 NIKISRLKVLTVVIVFYIYVLPYNIYKFCRAIDIIYSLTSCNMSKRMDAIQVTEFI 291
235 NFEHNKAIKVIAVVFVIFQLPYNGVLAQTVANFNITSTCLSKOLNADVTYSL 294
292 ALFHSCLNPLIYVFMGASFKNYVMKAKKYG-----SW-----RROQSVDEEPPD 337
295 ACVRCVNPFLIYAFIVKRNDFKLFKDLGCLSQEQLRWSSCHIRSSMSVE----- 349
338 SEGPTPEPTSTFS 349
350 ---AETTTTFS 357

RESULT 4
US-09-299-843A-19
Sequence 19, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848

FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 36.2%; Score 659; DB 3; Length 358;
Best Local Similarity 38.7%; Pred. No. 9,7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

1 MALEONOSTDYEEENMGTYDYOYELICEDVREFAKVLPVFLTVFVIGLAGNS 60
1 VCLQDEVDYDIGNT---TVDTLFEISCKKDVNFAMFLPIMYSIICFVGLGNG 57
61 MVAIYAYKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVGLKIMCKITSAIYT 120
58 LVVLYIYFKRKTMDTYLNLAVADILFTLPFAVNAVHGVGLKIMCKITSAIYT 117
121 LNFVSGMQLACISIDRYAVATKVP---QSGVGKPCWIIICVMAAILSIPLVFEY 176
118 MSFSGMQLLICTIDRYAIVQAVSAHRRARVLLISKSCVGIWILATVLSIPELLXS 177
177 TVNDNA-----RCIPFPRLGTSMKALIQMLEICIGFVPLMGVCYFITTARTLMKMP 231
178 DLQSSSEQAMRCSLITEH---VEAFITIQVQVGMVIGFLPLAMSFVYIITRLLOAR 234
232 NIKISRLKVLTVVIVFYIYVLPYNIYKFCRAIDIIYSLTSCNMSKRMDAIQVTEFI 291
235 NFEHNKAIKVIAVVFVIFQLPYNGVLAQTVANFNITSTCLSKOLNADVTYSL 294
292 ALFHSCLNPLIYVFMGASFKNYVMKAKKYG-----SW-----RROQSVDEEPPD 337
295 ACVRCVNPFLIYAFIVKRNDFKLFKDLGCLSQEQLRWSSCHIRSSMSVE----- 349
338 SEGPTPEPTSTFS 349
350 ---AETTTTFS 357

RESULT 5
US-09-088-337B-19
Sequence 19, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-088-337B-19

Query Match 36.2%; Score 659; DB 4; Length 358;
Best Local Similarity 38.7%; Pred. No. 9.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 M A L E B O N O S T D Y Y E N E N G T Y D Y S O Y E L I C I K E D V R E F A K V P L P V E L T I V F Y I G L A G N S 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 V C L O D E V T D Y I G D N T - - - T V D Y T L F E S L C S K R D V R N F K A M F L P I M S I I C F V G L L G N G 57

QY 61 M V A I A Y A Y K K O R K T D Y I I N L A V A D L L F T L P E A V A N V H G V G I K M C K I T S A L Y T 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 L V L V T Y I F K R L K T M T D Y L I N L A V A D I L F L T L P E A V S A K S M W E G V H C K L I F A I Y K 117

QY 121 L N F S G M O F L A C I S I D R V A V A T K V P S - - - O S G V K P C M I I C F C M M A A I L S I P O L E Y 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 M S F S G M L L C I S I D R V A V A V O A V S A H R H A R A V L L S K L S C V G I W I L A T V L S T P E L L Y S 177

QY 177 T V N D N A - - - R C I P I P R Y L G T S M K A L I O M L E I C I G F V P F L I M G V C Y F T A R T L M K M P 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 D L O R S S E Q A M R C S L I T E H - - - V E A F I T I Q V A Q W I G F L V P L L A M S C Y I V I I R T L L Q A R 234

QY 232 N I K I S R P L K V L I V Y I F Y T Q L P Y N I V K F C R A I D I I Y S L T S C M S K R M D I A I Q V E S I 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 N F E R N K A I K V I A V V V F I F O L P Y N G V L A Q T V A N F N I T S T C E L S K O L M I A D V Y S L 294

QY 292 A L F H S C L P I L Y V P M G A S F K Y V K V A K K Y G - - - S W - - - - - R R O R S V E E P P E D 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 A C V R C C V N P F L I A F I G K F R N D L F K L R D G C L S O E O L R O M S C R H I R R S M S V E - - - - - 349

QY 338 S E G P T E P T S F S 349
   : : : : :
Db 350 - - - - - A E T T T F S 357

RESULT 6
PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godtska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
```

```

;
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
PCT-US93-11153-19

Query Match 36.2%; Score 659; DB 5; Length 358;
Best Local Similarity 38.7%; Pred. No. 9.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 M A L B O N O S T D Y Y E N E N G T Y D Y S O Y E L I C I K E D V R E F A K V P L P V E L T I V F Y I G L A G N S 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 V C L O D E V T D Y I G D N T - - - T V D Y T L F E S L C S K R D V R N F K A M F L P I M S I I C F V G L L G N G 57

QY 61 M V A I A Y A Y K K O R K T D Y I I N L A V A D L L F T L P E A V A N V H G V G I K M C K I T S A L Y T 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 L V L V T Y I F K R L K T M T D Y L I N L A V A D I L F L T L P E A V S A K S M W E G V H C K L I F A I Y K 117

QY 121 L N F S G M O F L A C I S I D R V A V A T K V P S - - - O S G V K P C M I I C F C M M A A I L S I P O L E Y 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 M S F S G M L L C I S I D R V A V A V O A V S A H R H A R A V L L S K L S C V G I W I L A T V L S T P E L L Y S 177

QY 177 T V N D N A - - - R C I P I P R Y L G T S M K A L I O M L E I C I G F V P F L I M G V C Y F T A R T L M K M P 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 D L O R S S E Q A M R C S L I T E H - - - V E A F I T I Q V A Q W I G F L V P L L A M S C Y I V I I R T L L Q A R 234

QY 232 N I K I S R P L K V L I V Y I F Y T Q L P Y N I V K F C R A I D I I Y S L T S C M S K R M D I A I Q V E S I 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 N F E R N K A I K V I A V V V F I F O L P Y N G V L A Q T V A N F N I T S T C E L S K O L M I A D V Y S L 294

QY 292 A L F H S C L P I L Y V P M G A S F K Y V K V A K K Y G - - - S W - - - - - R R O R S V E E P P E D 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 A C V R C C V N P F L I A F I G K F R N D L F K L R D G C L S O E O L R O M S C R H I R R S M S V E - - - - - 349

QY 338 S E G P T E P T S F S 349
   : : : : :
Db 350 - - - - - A E T T T F S 357

RESULT 7
US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godtska, Ronald
```

APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-15

Query Match 36.2%; Score 659; DB 1; Length 378;
Best Local Similarity 38.7%; Pred. No. 1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALEONOSTDYEEENENMGTYDSQYELICIKEDVREFAKVLPVFLTIYFVIGLNGS 60
DB 21 VCLCODEVTDDYIGDNT---IVDTLFEISLCSKDVNRKFMFLPIMYSITICFVGLGNG 77
QY 61 MVAATYAYVKRQRTDVTYLLNLAVADLLFLTPFMAVNAHGVGLGKIMCKITSAIYT 120
DB 78 LVLTLYIFKRLKMTDVTYLLNLAVADLLFLTPFMAVSAKSWFVGHFCKLIFAIYK 137
QY 121 LNFVSGMQLACISIDRYVAATKVP-----QSGVGRKPCWITICFVMAAIIISIPOLVFY 176
DB 138 MSFSGMQLLCLSIDRYVAIVQAVSAHRARAVLLISKLCVGIWILATVLSIPELLYS 197
QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICIGFVFPFLINGCVFTFARTLMKMP 231
DB 198 DLORSSSQAMRCSLITEH---VEAFITIQVAGWVIGFVPLPILAMSCFYIIRILLQAR 254
QY 232 NIKISRLKVLITVIVIVITQLPYNIIVKFCRAIDIIYLSITSCMSKRDIAIQVTESTI 291
DB 255 NFERKKAIRKIVIAVVEFIVPOLPYNGVLAQTVANFNITSTCELSKOLNADVYSL 314
QY 292 ALPHSGCLNIIIVFMGASKKNVMAVKRYG-----SW-----RROQSVVEFFED 337
DB 315 ACVRCVNFELAFYGVAFKNDLFKFLDGLCLSOQLRQSSCRHRRSSMSVE----- 369
QY 338 SEGTEPTSTFS 349
DB 370 ----AETTTTFS 377

RESULT 8
US-09-299-843A-15
Sequence 15, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-15
Query Match 36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALEONOSTDYEEENENMGTYDSQYELICIKEDVREFAKVLPVFLTIYFVIGLNGS 60
DB 21 VCLCODEVTDDYIGDNT---IVDTLFEISLCSKDVNRKFMFLPIMYSITICFVGLGNG 77
QY 61 MVAATYAYVKRQRTDVTYLLNLAVADLLFLTPFMAVNAHGVGLGKIMCKITSAIYT 120
DB 78 LVLTLYIFKRLKMTDVTYLLNLAVADLLFLTPFMAVSAKSWFVGHFCKLIFAIYK 137
QY 121 LNFVSGMQLACISIDRYVAATKVP-----QSGVGRKPCWITICFVMAAIIISIPOLVFY 176
DB 138 MSFSGMQLLCLSIDRYVAIVQAVSAHRARAVLLISKLCVGIWILATVLSIPELLYS 197
QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICIGFVFPFLINGCVFTFARTLMKMP 231
DB 198 DLORSSSQAMRCSLITEH---VEAFITIQVAGWVIGFVPLPILAMSCFYIIRILLQAR 254
QY 232 NIKISRLKVLITVIVIVITQLPYNIIVKFCRAIDIIYLSITSCMSKRDIAIQVTESTI 291

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Db      255 NFERKAKIVIAVAVVIVFQLPYNGVLAQVAVANENITSTCELSQNLIAVDVYSL 314
Qy      292 ALFHSCNLPILYVFGASFKNVKAKKYG-----SW-----RROQSVEEPPD 337
Db      315 ACVRCVNPFLYAFIGVAFKFRNDLFKFKDGLGCLSOEQLRQWSSCRHRRSSMSVE----- 369
Qy      338 SEGTEPTSTPS 349
Db      370 -----AETTTTFS 377

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RESULT 9

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US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:
; APPLICANT: Edward R. Appelbaum
; APPLICANT: Henry M. Sarau
; APPLICANT: John R. White
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-251-545-1

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Query Match 36.2%; Score 659; DB 4; Length 378;

Best Local Similarity 38.7%; Pred. No. 1e-48;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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Qy      1  MLEBONOSTDYVEENENGTVDYISOYELICKEDEYREFAKVPFLPFLITVIFVIGLAGNS 60
Db      21  VCLQDEVTDDYIGDNT---TVDTYLFESLCSKKDVNFKAMFLPIMYSIICFVGLLNG 77
Qy      61  MVAATYAYKKORTKTDVYIINLAVALDLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120
Db      78  LVVLTYYFKRLKMTDTYLLNLAVADILFTLPFMAVSAKSWFGVHCKLIFALYK 137
Qy      121  LNFVSGMOFLACISIDRYVAIVATKVP-----OSGVKPCWIIICFCVMAAILLSIPOLVFY 176
Db      138  MSFSSGMLLICISIDRYVAIVQAVSAHRHARVLLISKSCVGIMLATVLSIPELLYS 197
Qy      177  TVNDNA-----RCIPFPRYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLMKP 231
Db      198  DLQSSSEQAMRCSLITEH---VEAFITIOVAQWIGFVLPLAMSCFYLVIRTLQAR 254
Qy      232  NIKISRPLKVLTVYIVFYIYQLPYNIYKFCRAIDIYLSITSCMSKRMADIAIOVTEST 291
Db      255  NFEENKAIKIVIAVAVVIVFQLPYNGVLAQVAVANENITSTCELSQNLIAVDVYSL 314
Qy      292  ALFHSCNLPILYVFGASFKNVKAKKYG-----SW-----RROQSVEEPPD 337
Db      315  ACVRCVNPFLYAFIGVAFKFRNDLFKFKDGLGCLSOEQLRQWSSCRHRRSSMSVE----- 369
Qy      338  SEGTEPTSTPS 349
Db      370  -----AETTTTFS 377

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RESULT 10
US-09-088-337B-15
; Sequence 15, Application US/09088337B
; Patent No. 6348574

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; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schwellkart, Vicki L.
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-088-337B-15

```

Query Match 36.2%; Score 659; DB 4; Length 378;

Best Local Similarity 38.7%; Pred. No. 1e-48;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

```

Qy      1  MLEBONOSTDYVEENENGTVDYISOYELICKEDEYREFAKVPFLPFLITVIFVIGLAGNS 60
Db      21  VCLQDEVTDDYIGDNT---TVDTYLFESLCSKKDVNFKAMFLPIMYSIICFVGLLNG 77
Qy      61  MVAATYAYKKORTKTDVYIINLAVALDLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120
Db      78  LVVLTYYFKRLKMTDTYLLNLAVADILFTLPFMAVSAKSWFGVHCKLIFALYK 137
Qy      121  LNFVSGMOFLACISIDRYVAIVATKVP-----OSGVKPCWIIICFCVMAAILLSIPOLVFY 176
Db      138  MSFSSGMLLICISIDRYVAIVQAVSAHRHARVLLISKSCVGIMLATVLSIPELLYS 197
Qy      177  TVNDNA-----RCIPFPRYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLMKP 231
Db      198  DLQSSSEQAMRCSLITEH---VEAFITIOVAQWIGFVLPLAMSCFYLVIRTLQAR 254
Qy      232  NIKISRPLKVLTVYIVFYIYQLPYNIYKFCRAIDIYLSITSCMSKRMADIAIOVTEST 291
Db      255  NFEENKAIKIVIAVAVVIVFQLPYNGVLAQVAVANENITSTCELSQNLIAVDVYSL 314
Qy      292  ALFHSCNLPILYVFGASFKNVKAKKYG-----SW-----RROQSVEEPPD 337
Db      315  ACVRCVNPFLYAFIGVAFKFRNDLFKFKDGLGCLSOEQLRQWSSCRHRRSSMSVE----- 369

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Db 230 DLORSSSEQAMRCSLITEH---VEAFITIOVAMVIGFLVPLPAMSFICYLVIIRTLLOAR 286
QY 232 NIKISRLKVLTVIVFIVTOLPYNYKFCRAIDIIYLSITSCNMKRMIDIAIOVTSI 291
Db 287 NERNKAIRKVIIVAVVVFIVFOLPYNGVLAOTVANFNITSTCJLSKOLNADIVTYSL 346
QY 292 ALFHSCNPLILVFMGASFKNVYKAKYK-----SW-----ROROSVEEFPD 337
Db 347 ACVRCVNPFLAFIGVKFRNDLFKFDLGLSOLRQMSCHIRRSSMSVE----- 401
QY 338 SEGPTEPTSTFS 349
Db 402 ---AETTTTFS 409
RESULT 13
US-09-299-843A-7
Sequence 7, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299, 843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088, 337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153, 848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977, 452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/320598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-7
Query Match 36.2%, Score 659, DB 3; Length 410;
Best Local Similarity 38.7%, Pred. No. 1,le-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
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Db 53 VCLQCDVETDIDYGDNT---TVDYTLFESLCSKQDVNRNFAKPLPIIMYSITICFVGLGNG 109
QY 61 MVAIVAYIKKQKRTKTVYILNLAADVLLFLPFAVAVAVGVULKMTCTALT 120
Db 110 LVVLTITFYFRKMTDITLLNLAVDILFLPLPFAVSAASWGVGFCKLIFAIVK 169
QY 121 LNFSGQPLACISIDRYVAVTVKPS---QSGVGKPCWITICFVMAAILISIPOLVY 176
Db 170 MFFSGMLLLCISIDRYVAVTVKPS---QSGVGKPCWITICFVMAAILISIPOLVY 229
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Db 230 DLORSSSEQAMRCSLITEH---VEAFITIOVAMVIGFLVPLPAMSFICYLVIIRTLLOAR 286
QY 232 NIKISRLKVLTVIVFIVTOLPYNYKFCRAIDIIYLSITSCNMKRMIDIAIOVTSI 291
Db 287 NERNKAIRKVIIVAVVVFIVFOLPYNGVLAOTVANFNITSTCJLSKOLNADIVTYSL 346
QY 292 ALFHSCNPLILVFMGASFKNVYKAKYK-----SW-----ROROSVEEFPD 337
Db 347 ACVRCVNPFLAFIGVKFRNDLFKFDLGLSOLRQMSCHIRRSSMSVE----- 401
QY 338 SEGPTEPTSTFS 349
Db 402 ---AETTTTFS 409

RESULT 14
US-09-088-337B-7
Sequence 7, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088, 337B
FILING DATE: 01-JUN-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153, 848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977, 452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-09-088-337B-7

Query Match 36.2%; Score 659; DB 4; Length 410;
Best Local Similarity 38.7%; Pred. No. 1.1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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DB 53 VCLCODEVTDDYIDGNT---TVDYTLFESLCSKKNVNRKAFLLIMVSIICFVGLLNG 109
QY 61 MVAIAYYKKORTKTDVYILMLAVADLLFLTPFWAVNAVHGVLGKIMCKITSALYT 120
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QY 121 LNFVSGMFLACISIDRYVAATKVP---QSGVGKPCMIICFCVMAAILSTPOLVFY 176
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QY 177 TVNDNA-----RCIPFPRLTGTSMKALIMLEICIGFVVPFLMGVCYFTRTLMKMP 231
DB 230 DLQSSSEQAMKCSLITEH---VEAFITQVAGVIGFVPLAMSCYLIITRTLLQAR 286
QY 232 NIKISRLKVLTVVIVFVITQLPYNIKFCRAIDIIYSLITSCNMSKRMIDAIOVTEST 291
DB 287 NFEENKAIVIAVVVFIYFQLPYNGVLAQTVANFNITSSTCELSKQNLNAYDVYSL 346
QY 292 ALFHSCLNPLIYVFMGASFKNYVMKAKYG-----SW-----RRROSVEEPPD 337
DB 347 ACYRCVNPFLYAFIVKFRNDLFKFDLGLCSQELRWMSCHIRSSMSVE----- 401
QY 338 SEGTEPTSTFS 349
DB 402 ----AETTTFS 409

RESULT 15
PCT-US93-11153-7
Sequence 7, Application PC/TUS9311153

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwaikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-7

Query Match 36.2%; Score 659; DB 5; Length 410;
Best Local Similarity 38.7%; Pred. No. 1.1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MAFONOSTDYEEENMGNGYDYSOYELICIKEDVREFAKVFLPVFLTVFVIGLAGNS 60
DB 53 VCLCODEVTDDYIDGNT---TVDYTLFESLCSKKNVNRKAFLLIMVSIICFVGLLNG 109
QY 61 MVAIAYYKKORTKTDVYILMLAVADLLFLTPFWAVNAVHGVLGKIMCKITSALYT 120
DB 110 LVLTLYIFKRLKMTDFTYLLMLAVADLLFLTPFWAVNAVHGVLGKIMCKITSALYT 169
QY 121 LNFVSGMFLACISIDRYVAATKVP---QSGVGKPCMIICFCVMAAILSTPOLVFY 176
DB 170 MSFSGMILLICISIDRYVAIVQAVSAHRHRAVLLISKSCVGIWILATVLSIPELLYS 229
QY 177 TVNDNA-----RCIPFPRLTGTSMKALIMLEICIGFVVPFLMGVCYFTRTLMKMP 231
DB 230 DLQSSSEQAMKCSLITEH---VEAFITQVAGVIGFVPLAMSCYLIITRTLLQAR 286
QY 232 NIKISRLKVLTVVIVFVITQLPYNIKFCRAIDIIYSLITSCNMSKRMIDAIOVTEST 291
DB 287 NFEENKAIVIAVVVFIYFQLPYNGVLAQTVANFNITSSTCELSKQNLNAYDVYSL 346
QY 292 ALFHSCLNPLIYVFMGASFKNYVMKAKYG-----SW-----RRROSVEEPPD 337
DB 347 ACYRCVNPFLYAFIVKFRNDLFKFDLGLCSQELRWMSCHIRSSMSVE----- 401
QY 338 SEGTEPTSTFS 349
DB 402 ----AETTTFS 409

Search completed: March 14, 2003, 16:12:09
Job time : 17 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:12:17 ; Search time 14 Seconds
(without alignments)
1152.302 Million cell updates/sec

Title: US-09-686-020a-2

Perfect score: 1819

Sequence: 1 MALEQNSQSDYYEENEMNG.....VEPPFDSGPTSTFSI 350

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Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications-AA*

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1819 | 100.0 | 350 | 10 | US-09-765-994-2 |
| 2 | 1819 | 100.0 | 350 | 10 | US-09-796-338A-8 |
| 3 | 1814 | 99.7 | 349 | 9 | US-09-765-994-4 |
| 4 | 761 | 41.8 | 175 | 9 | US-09-989-442-108 |
| 5 | 761 | 41.8 | 175 | 9 | US-10-073-865-91 |
| 6 | 761 | 41.8 | 175 | 10 | US-09-764-853-584 |
| 7 | 637 | 35.0 | 357 | 9 | US-09-966-755-2 |
| 8 | 637 | 35.0 | 357 | 10 | US-09-903-377-2 |
| 9 | 637 | 35.0 | 357 | 10 | US-09-952-385-2 |
| 10 | 637 | 35.0 | 357 | 12 | US-10-000-759A-2 |
| 11 | 581 | 31.9 | 342 | 10 | US-09-852-156-4 |
| 12 | 569 | 31.3 | 342 | 10 | US-09-852-156-6 |
| 13 | 560 | 30.8 | 342 | 10 | US-09-852-156-2 |
| 14 | 560 | 30.8 | 342 | 10 | US-09-940-063-2 |
| 15 | 537.5 | 29.5 | 360 | 9 | US-10-120-394-20 |
| 16 | 537.5 | 29.5 | 360 | 9 | US-09-764-413-20 |
| 17 | 537.5 | 29.5 | 360 | 10 | US-09-837-446-2 |
| 18 | 537.5 | 29.5 | 360 | 10 | US-09-796-744-17 |
| 19 | 532.5 | 29.3 | 360 | 10 | US-09-938-719-10 |

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| 20 | 532.5 | 29.3 | 360 | 10 | US-09-939-226-10 | Sequence 10, Appl |
| 21 | 532.5 | 29.3 | 360 | 10 | US-09-938-703-10 | Sequence 10, Appl |
| 22 | 526.5 | 28.9 | 362 | 10 | US-09-898-751A-4 | Sequence 4, Appl |
| 23 | 525 | 28.9 | 362 | 10 | US-09-931-381A-18 | Sequence 18, Appl |
| 24 | 522.5 | 28.7 | 355 | 10 | US-09-789-482-4 | Sequence 4, Appl |
| 25 | 522.5 | 28.7 | 355 | 10 | US-09-789-486-4 | Sequence 4, Appl |
| 26 | 518.5 | 28.5 | 362 | 9 | US-09-898-751A-2 | Sequence 2, Appl |
| 27 | 515.5 | 28.3 | 361 | 10 | US-09-931-381A-20 | Sequence 20, Appl |
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| 29 | 500.5 | 27.5 | 352 | 10 | US-09-953-692-2 | Sequence 2, Appl |
| 30 | 500.5 | 27.5 | 352 | 10 | US-09-953-117-2 | Sequence 2, Appl |
| 31 | 498.5 | 27.4 | 352 | 9 | US-09-870-759-37 | Sequence 37, Appl |
| 32 | 498.5 | 27.4 | 352 | 9 | US-09-870-759-144 | Sequence 144, App |
| 33 | 497 | 27.3 | 360 | 10 | US-09-938-719-7 | Sequence 7, Appl |
| 34 | 497 | 27.3 | 360 | 10 | US-09-939-226-7 | Sequence 7, Appl |
| 35 | 497 | 27.3 | 360 | 10 | US-09-938-703-7 | Sequence 7, Appl |
| 36 | 492 | 27.0 | 347 | 10 | US-09-104-792-3 | Sequence 3, Appl |
| 37 | 492 | 27.0 | 360 | 10 | US-09-131-827A-2 | Sequence 2, Appl |
| 38 | 491.5 | 27.0 | 352 | 12 | US-10-106-623-20 | Sequence 20, Appl |
| 39 | 491 | 27.0 | 360 | 10 | US-09-131-827A-20 | Sequence 20, Appl |
| 40 | 486.5 | 26.7 | 350 | 9 | US-09-104-063-2 | Sequence 2, Appl |
| 41 | 486.5 | 26.7 | 350 | 10 | US-09-782-980-83 | Sequence 83, Appl |
| 42 | 486.5 | 26.7 | 350 | 10 | US-09-884-430-7 | Sequence 7, Appl |
| 43 | 486 | 26.7 | 355 | 10 | US-09-104-792-2 | Sequence 2, Appl |
| 44 | 484.5 | 26.6 | 352 | 9 | US-10-232-666-2 | Sequence 2, Appl |
| 45 | 484.5 | 26.6 | 352 | 10 | US-09-725-285-2 | Sequence 2, Appl |

ALIGNMENTS

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| RESULT 1 | | | | | | | | | |
| US-09-765-994-2 | | | | | | | | | |
| ; Sequence 2, Application US/09765994 | | | | | | | | | |
| ; Patent No. US20010016336A1 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: ELLIS, CATHERINE | | | | | | | | | |
| ; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR | | | | | | | | | |
| ; FILE REFERENCE: GH-70225-C1 | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/765,994 | | | | | | | | | |
| ; CURRENT FILING DATE: 2001-01-19 | | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: 60/035,895 | | | | | | | | | |
| ; PRIOR FILING DATE: 1997-08-15 | | | | | | | | | |
| ; PRIOR APPLICATION NUMBER: 08/962,922 | | | | | | | | | |
| ; PRIOR FILING DATE: 1997-10-27 | | | | | | | | | |
| ; NUMBER OF SEQ ID NOS: 4 | | | | | | | | | |
| ; SOFTWARE: FastSeq for Windows Version 3.0 | | | | | | | | | |
| ; SEQ ID NO 2 | | | | | | | | | |
| ; LENGTH: 350 | | | | | | | | | |
| ; TYPE: PRT | | | | | | | | | |
| ; ORGANISM: HOMO SAPIENS | | | | | | | | | |
| US-09-765-994-2 | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 100.0%; Score 1819; DB 10; Length 350; | | | | | | | | | |
| Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
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| DB | 1 | MALEQNSQSDYYEENEMNGTDYD | SOYELICIKEDREFAKYFLPFLTIVIGLAGNS | 60 | | | | | |
| QY | 61 | MVAIAYKKKQTKTDYVTLNADV | LLFLTPMAVNAVHGVNIGKMKITSALYT | 120 | | | | | |
| DB | 61 | MVAIAYKKKQTKTDYVTLNADV | LLFLTPMAVNAVHGVNIGKMKITSALYT | 120 | | | | | |
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| DB | 121 | LNFSVGMQFLACISIDRYAVTV | VPSSQSGVGRKQWITICVMAAIIISIPOLVFTVND | 180 | | | | | |
| QY | 181 | NARCIPIFPYLTGSKKALQMLE | ICIGFVPLINGVCFYFARTLKMKNPKISRP | 240 | | | | | |
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RESULT 3
US-09-765-994-4
Sequence 4, Application US/09765994
Patent No. US2001001636A1
GENERAL INFORMATION:
APPLICANT: ELLIS, CATHERINE
TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
FILE REFERENCE: GH-70225-C1
CURRENT APPLICATION NUMBER: US/09/765,994
CURRENT FILING DATE: 2001-01-19
PRIORITY APPLICATION NUMBER: 60/055,895
PRIORITY FILING DATE: 1997-08-15

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RESULT 4
US-09-989-442-108
Sequence 108, Application US/09989442
Publication No. US20030013642A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P3208
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US/09/989,442
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/216,647
PRIOR FILING DATE: 2000-07-07

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| 1 | PRIOR APPLICATION NUMBER: 60/225,267 |
| 2 | PRIOR FILING DATE: 2000-08-14 |
| 3 | PRIOR APPLICATION NUMBER: 60/216,880 |
| 4 | PRIOR FILING DATE: 2000-07-07 |
| 5 | PRIOR APPLICATION NUMBER: 60/225,270 |
| 6 | PRIOR FILING DATE: 2000-08-14 |
| 7 | PRIOR APPLICATION NUMBER: 60/251,869 |
| 8 | PRIOR FILING DATE: 2000-12-08 |
| 9 | PRIOR APPLICATION NUMBER: 60/225,834 |
| 10 | PRIOR FILING DATE: 2000-09-27 |
| 11 | PRIOR APPLICATION NUMBER: 60/234,274 |
| 12 | PRIOR FILING DATE: 2000-09-21 |
| 13 | PRIOR APPLICATION NUMBER: 60/234,223 |
| 14 | PRIOR FILING DATE: 2000-09-21 |
| 15 | PRIOR APPLICATION NUMBER: 60/228,924 |
| 16 | PRIOR FILING DATE: 2000-08-30 |
| 17 | PRIOR APPLICATION NUMBER: 60/224,518 |
| 18 | PRIOR FILING DATE: 2000-08-14 |
| 19 | PRIOR APPLICATION NUMBER: 60/236,369 |
| 20 | PRIOR FILING DATE: 2000-09-29 |
| 21 | PRIOR APPLICATION NUMBER: 60/224,519 |
| 22 | PRIOR FILING DATE: 2000-08-14 |
| 23 | PRIOR APPLICATION NUMBER: 60/220,964 |
| 24 | PRIOR FILING DATE: 2000-07-26 |
| 25 | PRIOR APPLICATION NUMBER: 60/241,809 |
| 26 | PRIOR FILING DATE: 2000-10-20 |
| 27 | PRIOR APPLICATION NUMBER: 60/249,299 |
| 28 | PRIOR FILING DATE: 2000-11-17 |
| 29 | PRIOR APPLICATION NUMBER: 60/236,327 |
| 30 | PRIOR FILING DATE: 2000-09-29 |
| 31 | PRIOR APPLICATION NUMBER: 60/241,785 |
| 32 | PRIOR FILING DATE: 2000-10-20 |
| 33 | PRIOR APPLICATION NUMBER: 60/244,617 |
| 34 | PRIOR FILING DATE: 2000-11-01 |
| 35 | PRIOR APPLICATION NUMBER: 60/225,268 |
| 36 | PRIOR FILING DATE: 2000-08-14 |
| 37 | PRIOR APPLICATION NUMBER: 60/236,368 |
| 38 | PRIOR FILING DATE: 2000-09-29 |
| 39 | PRIOR APPLICATION NUMBER: 60/251,856 |
| 40 | PRIOR FILING DATE: 2000-12-08 |
| 41 | PRIOR APPLICATION NUMBER: 60/251,868 |
| 42 | PRIOR FILING DATE: 2000-12-08 |
| 43 | PRIOR APPLICATION NUMBER: 60/229,344 |
| 44 | PRIOR FILING DATE: 2000-09-01 |
| 45 | PRIOR APPLICATION NUMBER: 60/229,287 |
| 46 | PRIOR FILING DATE: 2000-09-01 |
| 47 | PRIOR APPLICATION NUMBER: 60/229,513 |
| 48 | PRIOR FILING DATE: 2000-09-05 |
| 49 | PRIOR APPLICATION NUMBER: 60/231,413 |
| 50 | PRIOR FILING DATE: 2000-09-08 |
| 51 | PRIOR APPLICATION NUMBER: 60/229,509 |
| 52 | PRIOR FILING DATE: 2000-09-05 |
| 53 | PRIOR APPLICATION NUMBER: 60/236,367 |
| 54 | PRIOR FILING DATE: 2000-09-29 |
| 55 | PRIOR APPLICATION NUMBER: 60/237,039 |
| 56 | PRIOR FILING DATE: 2000-10-02 |
| 57 | PRIOR APPLICATION NUMBER: 60/237,038 |
| 58 | PRIOR FILING DATE: 2000-10-02 |
| 59 | PRIOR APPLICATION NUMBER: 60/236,370 |
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| 61 | PRIOR APPLICATION NUMBER: 60/236,802 |
| 62 | PRIOR FILING DATE: 2000-10-02 |
| 63 | PRIOR APPLICATION NUMBER: 60/237,037 |
| 64 | PRIOR FILING DATE: 2000-10-02 |
| 65 | PRIOR APPLICATION NUMBER: 60/237,040 |
| 66 | PRIOR FILING DATE: 2000-10-02 |
| 67 | PRIOR APPLICATION NUMBER: 60/240,960 |

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| 3 | PRIOR FILING DATE: 2000-10-13 |
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| 8 | PRIOR APPLICATION NUMBER: 60/246, 474 |
| 9 | PRIOR FILING DATE: 2000-11-08 |
| 10 | PRIOR APPLICATION NUMBER: 60/246, 532 |
| 11 | PRIOR FILING DATE: 2000-11-08 |
| 12 | PRIOR APPLICATION NUMBER: 60/249, 216 |
| 13 | PRIOR FILING DATE: 2000-11-17 |
| 14 | PRIOR APPLICATION NUMBER: 60/249, 210 |
| 15 | PRIOR FILING DATE: 2000-11-17 |
| 16 | PRIOR APPLICATION NUMBER: 60/226, 661 |
| 17 | PRIOR FILING DATE: 2000-08-22 |
| 18 | PRIOR APPLICATION NUMBER: 60/225, 759 |
| 19 | PRIOR FILING DATE: 2000-08-14 |
| 20 | PRIOR APPLICATION NUMBER: 60/225, 213 |
| 21 | PRIOR FILING DATE: 2000-08-14 |
| 22 | PRIOR APPLICATION NUMBER: 60/227, 182 |
| 23 | PRIOR FILING DATE: 2000-08-22 |
| 24 | PRIOR APPLICATION NUMBER: 60/225, 214 |
| 25 | PRIOR FILING DATE: 2000-08-14 |
| 26 | PRIOR APPLICATION NUMBER: 60/235, 836 |
| 27 | PRIOR FILING DATE: 2000-09-27 |
| 28 | PRIOR APPLICATION NUMBER: 60/230, 438 |
| 29 | PRIOR FILING DATE: 2000-09-06 |
| 30 | PRIOR APPLICATION NUMBER: 60/215, 135 |
| 31 | PRIOR FILING DATE: 2000-06-30 |
| 32 | PRIOR APPLICATION NUMBER: 60/225, 266 |
| 33 | PRIOR FILING DATE: 2000-08-14 |
| 34 | PRIOR APPLICATION NUMBER: 60/249, 218 |
| 35 | PRIOR FILING DATE: 2000-11-17 |
| 36 | PRIOR APPLICATION NUMBER: 60/249, 208 |
| 37 | PRIOR FILING DATE: 2000-11-17 |
| 38 | PRIOR APPLICATION NUMBER: 60/249, 213 |
| 39 | PRIOR FILING DATE: 2000-11-17 |
| 40 | PRIOR APPLICATION NUMBER: 60/249, 212 |
| 41 | PRIOR FILING DATE: 2000-11-17 |
| 42 | PRIOR APPLICATION NUMBER: 60/249, 207 |
| 43 | PRIOR FILING DATE: 2000-11-17 |
| 44 | PRIOR APPLICATION NUMBER: 60/249, 245 |
| 45 | PRIOR FILING DATE: 2000-11-17 |
| 46 | PRIOR APPLICATION NUMBER: 60/249, 244 |
| 47 | PRIOR FILING DATE: 2000-11-17 |
| 48 | PRIOR APPLICATION NUMBER: 60/249, 217 |
| 49 | PRIOR FILING DATE: 2000-11-17 |
| 50 | PRIOR APPLICATION NUMBER: 60/249, 211 |
| 51 | PRIOR FILING DATE: 2000-11-17 |
| 52 | PRIOR APPLICATION NUMBER: 60/249, 215 |
| 53 | PRIOR FILING DATE: 2000-11-17 |
| 54 | PRIOR APPLICATION NUMBER: 60/249, 264 |
| 55 | PRIOR FILING DATE: 2000-11-17 |
| 56 | PRIOR APPLICATION NUMBER: 60/249, 214 |
| 57 | PRIOR FILING DATE: 2000-11-17 |
| 58 | PRIOR APPLICATION NUMBER: 60/249, 297 |
| 59 | PRIOR FILING DATE: 2000-11-17 |
| 60 | PRIOR APPLICATION NUMBER: 60/232, 4000 |
| 61 | PRIOR FILING DATE: 2000-09-14 |
| 62 | PRIOR APPLICATION NUMBER: 60/231, 242 |
| 63 | PRIOR FILING DATE: 2000-09-08 |
| 64 | PRIOR APPLICATION NUMBER: 60/232, 081 |
| 65 | PRIOR FILING DATE: 2000-09-08 |
| 66 | PRIOR APPLICATION NUMBER: 60/232, 080 |
| 67 | PRIOR FILING DATE: 2000-09-08 |
| 68 | PRIOR APPLICATION NUMBER: 60/231, 414 |
| 69 | PRIOR FILING DATE: 2000-09-08 |
| 70 | PRIOR APPLICATION NUMBER: 60/231, 244 |
| 71 | PRIOR FILING DATE: 2000-09-08 |
| 72 | PRIOR APPLICATION NUMBER: 60/233, 064 |
| 73 | PRIOR FILING DATE: 2000-09-14 |

;; PRIOR APPLICATION NUMBER: 60/233,063
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,397
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,399
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,401
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,826
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/231,243
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,065
;; PRIOR FILING DATE: 2000-09-14

Query Match 41.8%; Score 761; DB 9; Length 175;
Best Local Similarity 96.1%; Pred. No. 5, Le-60;
Matches 148; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 197 KALLOMLEICIGFVVPFLMGVCYFRTARTLKMKNIKISRPKLVLTVVIVFIVTOLPY 256
DB 22 ESIDSMLEICIGFVVPFLMGVCYFRTERTLKMKNIKISRPKLVLTVVIVFIVTOLPY 81
QY 257 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 316
DB 82 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 141
QY 317 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 350
DB 142 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 175

RESULT 5
US-10-073-865-91
;; Sequence 91, Application US/10073865
;; Publication No. US20030044904A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PJ209C1
;; CURRENT APPLICATION NUMBER: US/10/073,865
;; CURRENT FILING DATE: 2002-02-14
;; Prior Application removed - See file wrapper or Palm
;; NUMBER OF SEQ ID NOS: 154
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 91
;; LENGTH: 175
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (16)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: misc_feature
;; LOCATION: (19)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-073-865-91

Query Match 41.8%; Score 761; DB 9; Length 175;
Best Local Similarity 96.1%; Pred. No. 5, Le-60;
Matches 148; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 197 KALLOMLEICIGFVVPFLMGVCYFRTARTLKMKNIKISRPKLVLTVVIVFIVTOLPY 256
DB 22 ESIDSMLEICIGFVVPFLMGVCYFRTERTLKMKNIKISRPKLVLTVVIVFIVTOLPY 81

QY 257 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 316
DB 82 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 141
QY 317 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 350
DB 142 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 175

RESULT 6
US-09-764-853-584
;; Sequence 584, Application US/09764853
;; Patent No. US20020090672A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PJ206
;; CURRENT APPLICATION NUMBER: US/09/764,853
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 939
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 584
;; LENGTH: 175
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (16)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (19)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-584

Query Match 41.8%; Score 761; DB 10; Length 175;
Best Local Similarity 96.1%; Pred. No. 5, Le-60;
Matches 148; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 197 KALLOMLEICIGFVVPFLMGVCYFRTARTLKMKNIKISRPKLVLTVVIVFIVTOLPY 256
DB 22 ESIDSMLEICIGFVVPFLMGVCYFRTERTLKMKNIKISRPKLVLTVVIVFIVTOLPY 81
QY 257 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 316
DB 82 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 141
QY 317 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 350
DB 142 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 175

RESULT 7
US-09-966-755-2
;; Sequence 2, Application US/09966755
;; Publication No. US2003002238A1
;; GENERAL INFORMATION:
;; APPLICANT: Andrew, David P.
;; APPLICANT: Zabel, Brian A.
;; APPLICANT: Ponath, Paul D.
;; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
;; IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
;; FILE REFERENCE: LKS98-16
;; CURRENT APPLICATION NUMBER: US/09/966,755
;; CURRENT FILING DATE: 2001-09-28
;; PRIOR APPLICATION NUMBER: US/09/266,464
;; PRIOR FILING DATE: 1999-03-11
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 357
;; TYPE: PRT

ORGANISM: Homo sapiens
US-09-966-753-2

Query Match 35.0%; Score 637; DB 9; Length 357;
Best Local Similarity 36.5%; Pred. No. 1e-48;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DRYEE-NEANGTYDSQVELICKEDEYREFAKVLPVFLTYFVIGLAGNSMVAIYAY 68
DB 4 DYSESTSMEDYVNFETDCEKNNVROFASHFLPPLXWLVFVIGLAGNSLVILVYVY 63
QY 69 YKQRTKTDVYIILNLAADLLFTLPFWAVNAHVGLKIMCKITSAIYTLNFSVGMQ 128
DB 64 CTRKVTMTDFLNLALADLLFTLVLPFWAIAADQMKPOTFMCKVYNSMYKNFYSCVL 123
QY 129 FLACISIDRYVAATKVPSSQSGVGRPCW-----IICFCVMAAILSLPOLVFTYV 179
DB 124 LIMCISVDRYIAIAQ-----AMRAHTWREKRLLYSKMVCFTIWLAAALCIPILYSQIK 178
QY 180 DN---ARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTIARTIMKPNIKIS 236
DB 179 EESGIAICTMVPDSDESKLSAVLTILKVLGFLFPVWACCTIIITHLIAKSSKH 238
QY 237 RPLKVLTVVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMRMDIAIQTESIAPHS 296
DB 239 KALKVTITVLVFLVLSQFPYNCILLVOTIDAYAMFISNCAVSTNDICFQVOTIAFHS 298
QY 297 CLNPILYFVGASFKNYVMAKAYG 322
DB 299 CLNPVLVYFVGERRRDLVTKLNLG 324

RESULT 8

US-09-903-377-2
Sequence 2, Application US/09903377
Patent No. US20020116727A1

GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
TITLE OF INVENTION: RECEPTOR 9A GENE DISRUPTIONS
FILE REFERENCE: R-365
CURRENT APPLICATION NUMBER: US/09/903,377
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/217,255
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/221,483
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/262,113
PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Targeting vector
US-09-903-377-2

Query Match 35.0%; Score 637; DB 10; Length 357;
Best Local Similarity 36.5%; Pred. No. 1e-48;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DRYEE-NEANGTYDSQVELICKEDEYREFAKVLPVFLTYFVIGLAGNSMVAIYAY 68
DB 4 DYSESTSMEDYVNFETDCEKNNVROFASHFLPPLXWLVFVIGLAGNSLVILVYVY 63
QY 69 YKQRTKTDVYIILNLAADLLFTLPFWAVNAHVGLKIMCKITSAIYTLNFSVGMQ 128
DB 64 CTRKVTMTDFLNLALADLLFTLVLPFWAIAADQMKPOTFMCKVYNSMYKNFYSCVL 123
QY 129 FLACISIDRYVAATKVPSSQSGVGRPCW-----IICFCVMAAILSLPOLVFTYV 179
DB 124 LIMCISVDRYIAIAQ-----AMRAHTWREKRLLYSKMVCFTIWLAAALCIPILYSQIK 178

DB 124 LIMCISVDRYIAIAQ-----AMRAHTWREKRLLYSKMVCFTIWLAAALCIPILYSQIK 178
QY 180 DN---ARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTIARTIMKPNIKIS 236
DB 179 EESGIAICTMVPDSDESKLSAVLTILKVLGFLFPVWACCTIIITHLIAKSSKH 238
QY 237 RPLKVLTVVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMRMDIAIQTESIAPHS 296
DB 239 KALKVTITVLVFLVLSQFPYNCILLVOTIDAYAMFISNCAVSTNDICFQVOTIAFHS 298
QY 297 CLNPILYFVGASFKNYVMAKAYG 322
DB 299 CLNPVLVYFVGERRRDLVTKLNLG 324

RESULT 9

US-09-952-385-2
Sequence 2, Application US/09952385
Patent No. US20020119504A1

GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
FILE REFERENCE: LKS98-16
CURRENT APPLICATION NUMBER: US/09/952,385
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-952-385-2

Query Match 35.0%; Score 637; DB 10; Length 357;
Best Local Similarity 36.5%; Pred. No. 1e-48;
Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DRYEE-NEANGTYDSQVELICKEDEYREFAKVLPVFLTYFVIGLAGNSMVAIYAY 68
DB 4 DYSESTSMEDYVNFETDCEKNNVROFASHFLPPLXWLVFVIGLAGNSLVILVYVY 63
QY 69 YKQRTKTDVYIILNLAADLLFTLPFWAVNAHVGLKIMCKITSAIYTLNFSVGMQ 128
DB 64 CTRKVTMTDFLNLALADLLFTLVLPFWAIAADQMKPOTFMCKVYNSMYKNFYSCVL 123
QY 129 FLACISIDRYVAATKVPSSQSGVGRPCW-----IICFCVMAAILSLPOLVFTYV 179
DB 124 LIMCISVDRYIAIAQ-----AMRAHTWREKRLLYSKMVCFTIWLAAALCIPILYSQIK 178
QY 180 DN---ARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTIARTIMKPNIKIS 236
DB 179 EESGIAICTMVPDSDESKLSAVLTILKVLGFLFPVWACCTIIITHLIAKSSKH 238
QY 237 RPLKVLTVVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMRMDIAIQTESIAPHS 296
DB 239 KALKVTITVLVFLVLSQFPYNCILLVOTIDAYAMFISNCAVSTNDICFQVOTIAFHS 298
QY 297 CLNPILYFVGASFKNYVMAKAYG 322
DB 299 CLNPVLVYFVGERRRDLVTKLNLG 324

RESULT 10

US-10-000-759A-2
Sequence 2, Application US/10000759A
Patent No. US20020141991A1

GENERAL INFORMATION:
APPLICANT: Andrew, David P.

APPLICANT: Zabel, Brian A.
 APPLICANT: Ponath, Paul D.
 TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
 IDENTIFYING MODULATORS OF GPR-9-6 FUNCTION
 FILE REFERENCE: 1855,1064-003
 CURRENT APPLICATION NUMBER: US/10/000,759A
 CURRENT FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: US/09/522,752
 PRIOR FILING DATE: 2000-05-10
 PRIOR APPLICATION NUMBER: US 09/266,464
 PRIOR FILING DATE: 1999-03-11
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSeq for windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 357
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-000-759A-2

Query Match 35.0%; Score 637; DB 12; Length 357;
 Best Local Similarity 36.5%; Pred. No. 1e-48;
 Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

QY 10 DYEE-NEKNGTDDYSEYELICKEDEVEFAKFLPVELTIVFVIGLAGNSMVAIYAY 68
 DB 4 DYSESTSSMEDYVNFNFDYCEKNNVROFASHFLPLXWLVFVIGLAGNSLVLIYWF 63
 QY 69 YKORRTDYIILNLAVALDLEFLPEMAVNAHGVWLGKIMCKITSAVTLNPFVSGMO 128
 DB 64 CTWKTMTDMLFLNLAIDLFLVLPFMAIAADQMKFOTPECKVNVNMYKMFYSCVL 123
 QY 129 FLACISIDRYAVATKVPSSGSGKPCW-----IICFCVMAAIIISIPQVLYTVN 179
 DB 124 LINCISVDRIATAQ-----ANAHMTWREKRLIYSKMCVFTIWLAAALCIEPILYSQIK 178
 QY 180 DN---ARCIPIEFRLYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLKMNIKIS 236
 DB 179 EESGAICTMVVPSDESTKLSAVLTLKGLPFLPFVVMACCYITIIHTLQAKKSSKH 238
 QY 237 RPLKVLIVVIVYIQLRYNYKFCRAIDIIYSLTSCNMSKRDIAIQVTESTALPHS 296
 DB 239 KAKVITIVLVVLSQFPYNCILLVOTIDAYAMFISNCVSTNIDICQVOTIAFFHS 298
 QY 297 CLNPILYFMGASFKNYKMKVAKKYG 322
 DB 299 CLNPIYLYFVGERRRDLVKTAKNG 324

RESULT 11

US-09-852-156-4
 Sequence 4, Application US/09852156
 Patent No. US20020076694A1

GENERAL INFORMATION:

APPLICANT: Liltman, Dan R.

Deng, Hongkui
 Untmaz, Derya
 Ramanul, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS

ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/852,156
 FILING DATE: 09-May-2001
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 342 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: African Green Monkey
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-852-156-4

Query Match 31.9%; Score 581; DB 10; Length 342;
 Best Local Similarity 34.2%; Pred. No. 8.2e-44;
 Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps 8;

QY 12 YEEENMGNTDYSEYELICKEDEVEFAKFLPVELTIVFVIGLAGNSMVAIYAYK 71
 DB 6 HYEDGFNSFNDSSQOE---HODELOFSKVELPCMLVVFVCGLVGNSLVLSIFYHK 61
 QY 72 ORTKTDVYIILNLAVALDLEFLPEMAVNAHGVWLGKIMCKITSAVTLNPFVSGMOFLA 131
 DB 62 LOSLDFVFLVNLPLADLVFVCTLPFMAVAGCHEHIFQVCKITLIGTYITNFTSMILIT 121
 QY 132 CISIDRYAVATKVPSSGSGKPCW-----IICFCVMAAIIISIPQVLYTVN--NDNARCT 185
 DB 122 CTVDFRFLVAVKATKAVNOQAKKMTGKVICLLIWLIVSLVSLPQITIGVAVFLDKLIC- 180
 QY 186 PIFRPLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLKMNIKISRPLKVLTV 245
 DB 181 ---GYHDEISTVLAQTQMLGFLPLAMICYSVIITLLHAGGFQHRSLKTIIFLV 236
 QY 246 VIVEFIVQLPNIYKFCRAIDIIYSLTSCNMSKRDIAIQVTESTALPHSCNPILYVF 305
 DB 237 MAVFLITQTPENLVKLRSTHWEYAMTSFHYT-----IIVTEALIVLACLNPILYAF 290
 QY 306 MGASFKNYKMKVAKKYG-----SWROROSVEEFPDSDGPEPTSTFSI 350
 DB 291 VSLKFRKNFMKLVKDICLPLVGLVSHQWKSSEDSNK--TFASAHNVEATSMFOL 342

RESULT 12

US-09-852-156-6
 Sequence 6, Application US/09852156
 Patent No. US20020076694A1

GENERAL INFORMATION:

APPLICANT: Liltman, Dan R.

Deng, Hongkui
 Untmaz, Derya
 Ramanul, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS

ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor

```

      IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
      THEREOF
      NUMBER OF SEQUENCES: 20
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: David A. Jackson, Esq.
      STREET: 411 Hackensack Ave, Continental Plaza, 4th
              Floor
      CITY: Hackensack
      STATE: New Jersey
      COUNTRY: USA
      ZIP: 07601
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent In Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      FILING DATE: 09-May-2001
      CLASSIFICATION: <Unknown>
      ATTORNEY/AGENT INFORMATION:
      NAME: Jackson Esq., David A.
      REGISTRATION NUMBER: 26,742
      REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 201-487-5800
      TELEFAX: 201-343-1684
      INFORMATION FOR SEQ ID NO: 2:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 342 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      HYPOTHEetical: NO
      ORIGINAL SOURCE:
      ORGANISM: Homo sapiens
      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-852-156-2
Query Match          30.8%; Score 560; DB 10; Length 342;
Best Local Similarity 33.1%; Pred. No. 5,9e-42;
Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;
QY    12 YYENEMNGTVDSOYELTICKEDYREFAKVFLPVLITVEVIGLAGSNMVAIAYYYKK 71
       :|:::| | | | | :|:::||||| :||| |||||:|:| |
Db     6 YHEDGFSSFNDSOE---HDFLOFSKVFLPCMYLVGFCGLGNSLVVISIFYHK 61
       ::||:::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    72 ORTKTDVYLILAAVDLILLFTLPKMAVNAAHWGIKIMCKITSALTYLTINPVSMOLA 131
       ::||:::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     62 LOSLDVFLVNLPLADLVLCCTLPMAIAGIHENVFGVMCKSLGITVINPYTSMILT 121
       :|:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    132 CISIDRYAVAVRVKS--OSGVGKPCM--IICFCVMAAIIISLPDLVFYTV--NDMARCI 185
       ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     122 CIYDRFLIVVAKRANYNQAKRMWGWKVTSLLIWVISLSVSPQIIGVNFMDKLIC- 180
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    186 PIFPRYLTISKALIOMLEICGFVPPLMGVCYCFITARTLMKPNIKISRPLKVLTV 245
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     181 ---GYHDEAIISTVVLAOTMLTGFFLLPLTMIVCVSVIIKTLLHAGGFOKHRSLKITPLY 236
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    246 VIVEFVTDLPINIVKFCRAIDIYSLTSCNMKSRMDAIOVESIALFHSCLNPILVVF 305
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     237 MAVELLTOMPKNMKFIISTHMEYAMTSPIYT-----INVTEIAIIRACLNPPVLAFA 290
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    306 MGASFKNIVKVAKKYG-----SWRRORSVEEFPDSEGEPTSTPSI 350
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     291 VSLFRKFMWLIVKDIGCLPYLGVSHOWKSSSEDNSK--TFASAHVNEATSMFOL 342

```

```

: GENERAL INFORMATION:
: APPLICANT: Briskin, Michael J.
: APPLICANT: Murphy, Kristine E.
: APPLICANT: Wilbanks, Alyson M.
: APPLICANT: Wu, Lijun
: TITLE OF INVENTION: No. US20020090657A1el Antibodies and Ligands for "Bonzo"
: FILE OF INVENTION: Chemokine Receptor
: FILE REFERENCE: 1855.1070-000
: CURRENT APPLICATION NUMBER: US/09/940,063
: CURRENT FILING DATE: 2001-08-27
: PRIOR APPLICATION NUMBER: 09/449,437
: PRIOR FILING DATE: 1999-11-24
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 342
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-940-063-2

```

```

Query Match          30.8%; Score 560; DB 10; Length 342;
Best Local Similarity 33.1%; Pred. No. 5,9e-42;
Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

```

```

QY 12 YEEENENNGTYDYSQYELICKEDEYREFAKVFLEPFLTYFVIGLAGNSWVAIYAYK 71
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 YHEYGESEFNDSSQEE---HDFLQFSKVFLEPCMYLVFVCGLVGNSVLVLSIFYHK 61

QY 72 QRTQTDVYILNLAVADLLFTLPEMAVNAVHGVNLGKIMCKITSAIYTLNPFSGMOFLA 131
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 LQSLTDVFLVNLPLADLVFVCTLPFMAIYAGIHEWFGQVCKSLGLGTYTTFNFTSMILT 121

QY 132 CISIDRYAVATKVS--QSQVGKPCW--IICFCVMAAILLSIPOLVFYV--NDNARCI 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 CITVDREIVVYKATKAVNOQAKRMWTKGVTSLIIVISLVSPQIITGVNFDKILIC- 180

QY 186 PIFRPIYLGTSKALIQMLEICIGFVVPFLMGVCYFTIARTLMKMPRIKISRPKVLIV 245
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 ---GYDEALSTVLAIVLQMTLGFPLPLTMYCYSVIITKLLHAGGFGKHRSKILFIV 236

QY 246 VIVEIVTQLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIOVTESIALFHSCLNPLIYV 305
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 MAVFLTLQMPENLMKFTIRSTHWEYAMTSFHYT-----IMVTAIYVLAACLNPIYAT 290

QY 306 MGASFKNYVMKVKARYG-----SWRRQROSVEEFPDSGPTPEPTSTFSI 350
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 VSLFRKRMFKLVKIDICLPYLGVSQHWKXSEDSNK--TFSSHNVVATSMFOL 342

```

```

RESULT 15
US-10-120-394-20
: Sequence 20, Application US/10120394
: Patent No. US20020160015A1

```

GENERAL INFORMATION:

APPLICANT: Wells, Timothy N.C.

APPLICANT: Power, Christine A.

TITLE OF INVENTION: CHEMOKINE RECEPTOR ABLE TO BIND TO

MCP-1, MIP-1 ALPHA AND/OR RANTES AND ITS USES

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHIE P.C.

STREET: 1100 NO. US20020160015Alth Glebe Rd. 8th floor

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/120,394

```

: FILING DATE: 12-Apr-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/614,256
: FILING DATE: 12-JUL-2000
: APPLICATION NUMBER: US 08/875,573
: FILING DATE: 31-OCT-1997
: APPLICATION NUMBER: PCT/GB96/00143
: FILING DATE: 24-JAN-1996
: APPLICATION NUMBER: GB 9501683.8
: FILING DATE: 27-JAN-1995
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 360 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-120-394-20

```

```

Query Match          29.5%; Score 537.5; DB 9; Length 360;
Best Local Similarity 35.8%; Pred. No. 6e-40;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

```

```

QY 10 DYIYENENNGTYDYSQYELICKEDEYREFAKVFLEPFLTYFVIGLAGNSWVAIYAY 69
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 DTLDESISYNNYLYESIPKPCCKEIKAFGLFLPPLYSIVFVGLGNSVYLVLEKY 67

QY 70 KQRTQTDVYILNLAVADLLFTLPEMAVNAVHGVNLGKIMCKITSAIYTLNPFSGMOF 129
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 KRLRSMTDYLNLALSDLVFVSLPFGCYTAADQWVGLGCKMISWYLVGFSGIIF 127

QY 130 LACISIDRYAVATKVS-----PSQVGKPCWIIICFCVMAAILLSIPOLVF--YTVN 179
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 VMLMSIDRYALIVHAFSLRARTLTGYV-----ITSLTWASVAVPASPGLFSTCYTER 182

QY 180 DNARCIPIFRPIYLGTSKALIQMLEI-CIGFVVPFLMGVCYFTIARTLMKMPRIKISRP 238
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 NHYCKTKYS--LNSTWVKVLSLEINILGLVPLGIMLFCYSMLIRLQHCNKKRKA 240

QY 239 LKVLIVVIVTQLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIOVTESIALFHSCL 298
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 VKMIFVAVVLFGLFMPYIVIVLETL--VELEVLDCCIFERYLDAIQAETLAVHCL 299

QY 299 NPLIYVFMGASFKNYVMKVKAK 319
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 NPLIYFELGEKFRKYLQLFK 320

```

```

Search completed: March 14, 2003, 16:16:55
Job time : 16 secs

```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 16:11:03 ; Search time 32 Seconds

(without alignments)
2253.640 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819
Sequence: 1 MALEONQSTDDYEEENEMNG.....VEEPPDSGPTPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organella:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|-------------------------|
| 1 | 1596 | 87.7 | 350 | 11 Q92413 | Q92413 mus musculus |
| 2 | 1593 | 87.6 | 350 | 11 Q802W9 | Q802W9 mus musculus |
| 3 | 912 | 50.1 | 221 | 11 Q9ESK1 | Q9ESK1 rat mus musculus |
| 4 | 643 | 35.3 | 369 | 4 Q9U006 | Q9U006 homo sapien |
| 5 | 611 | 33.6 | 367 | 11 Q9R1V0 | Q9R1V0 mus musculus |
| 6 | 586.5 | 32.2 | 368 | 13 Q42444 | Q42444 oncorhynch |
| 7 | 578 | 31.8 | 343 | 6 Q9N020 | Q9N020 cercocebus |
| 8 | 566.5 | 31.1 | 351 | 11 Q9E016 | Q9E016 mus musculus |
| 9 | 566 | 31.1 | 343 | 6 Q9B056 | Q9B056 macaca fasc |
| 10 | 561.5 | 30.9 | 351 | 11 Q9ERH5 | Q9ERH5 mus musculus |
| 11 | 560 | 30.8 | 342 | 4 Q9HCA5 | Q9HCA5 homo sapien |
| 12 | 559 | 30.7 | 342 | 6 Q9TV16 | Q9TV16 pan troglod |
| 13 | 544 | 29.9 | 358 | 13 Q9PUA0 | Q9PUA0 acipenser r |
| 14 | 534.5 | 29.4 | 360 | 11 Q912H4 | Q912H4 rattus norv |
| 15 | 529 | 29.1 | 361 | 11 Q8VHP3 | Q8VHP3 cavia porce |
| 16 | 520.5 | 28.6 | 358 | 13 Q9YGC3 | Q9YGC3 xenopus lae |

| | | | | | |
|----|-------|------|-----|-----------|---------------------|
| 17 | 516 | 28.4 | 355 | 11 Q9JLX8 | Q9JLX8 rattus norv |
| 18 | 507.5 | 27.9 | 347 | 6 Q9MZM1 | Q9MZM1 eulemur mac |
| 19 | 507 | 27.9 | 357 | 13 Q42445 | Q42445 oncorhynch |
| 20 | 506.5 | 27.8 | 347 | 6 Q9MZM7 | Q9MZM7 callimico g |
| 21 | 506.5 | 27.8 | 347 | 6 Q9MZM6 | Q9MZM6 callimico g |
| 22 | 503.5 | 27.7 | 347 | 6 Q9MZM0 | Q9MZM0 alouatta se |
| 23 | 503.5 | 27.7 | 352 | 6 Q9V444 | Q9V444 cercopithec |
| 24 | 502.5 | 27.6 | 347 | 6 Q9MZP1 | Q9MZP1 mandrillus |
| 25 | 502.5 | 27.6 | 347 | 6 Q9MZM9 | Q9MZM9 atelapha pan |
| 26 | 502.5 | 27.6 | 347 | 6 Q9MZM8 | Q9MZM8 callithrix |
| 27 | 502.5 | 27.6 | 347 | 6 Q9MZM5 | Q9MZM5 pithecia pi |
| 28 | 500.5 | 27.5 | 347 | 6 Q9MZM6 | Q9MZM6 presbytis j |
| 29 | 500.5 | 27.5 | 347 | 6 Q9MZM6 | Q9MZM6 hylobates c |
| 30 | 500.5 | 27.5 | 347 | 6 Q9MZM5 | Q9MZM5 hylobates h |
| 31 | 500.5 | 27.5 | 347 | 6 Q9MZM2 | Q9MZM2 ponga pygma |
| 32 | 500.5 | 27.5 | 347 | 6 Q9MZM1 | Q9MZM1 gorilla gor |
| 33 | 500.5 | 27.5 | 352 | 6 Q9TS08 | Q9TS08 cercopithec |
| 34 | 499.5 | 27.5 | 339 | 6 Q9TUR8 | Q9TUR8 cercopithec |
| 35 | 499.5 | 27.5 | 339 | 6 Q9TUR4 | Q9TUR4 mandrillus |
| 36 | 499.5 | 27.5 | 347 | 6 Q9MZ03 | Q9MZ03 pygathrix a |
| 37 | 499.5 | 27.5 | 347 | 6 Q9MZ02 | Q9MZ02 rhinopithec |
| 38 | 499.5 | 27.5 | 347 | 6 Q9MZ01 | Q9MZ01 pygathrix b |
| 39 | 499.5 | 27.5 | 347 | 6 Q9MZ00 | Q9MZ00 pygathrix n |
| 40 | 499.5 | 27.5 | 347 | 6 Q9MZP9 | Q9MZP9 nasalis lar |
| 41 | 499.5 | 27.5 | 347 | 6 Q9MZP8 | Q9MZP8 colobus pol |
| 42 | 499.5 | 27.5 | 347 | 6 Q9MZP5 | Q9MZP5 presbytis p |
| 43 | 499.5 | 27.5 | 347 | 6 Q9MZP4 | Q9MZP4 presbytis f |
| 44 | 499.5 | 27.5 | 347 | 6 Q9MZP3 | Q9MZP3 presbytis e |
| 45 | 499.5 | 27.5 | 347 | 6 Q9MZP2 | Q9MZP2 mandrillus |

ALIGNMENTS

RESULT 1

| ID | Q92413 | PRELIMINARY: | PRT: | 350 AA. |
|----|---|--------------|------|---------|
| AC | Q92413 | Q92413 | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Created) | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | | |
| DE | Chemokine receptor CCR11. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=BALE/C; | | | |
| RX | MEDLINE=20519697; PubMed=11063828; | | | |
| RA | Dorf M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.; | | | |
| RT | "Astrocytes express functional chemokine receptors."; | | | |
| RL | J. Neuroimmunol. 111:109-121(2000). | | | |
| DR | EMBL: AF306532; AAK81712.1; - | | | |
| DR | InterPro: IPR000276; GPCR_Rhodpsn. | | | |
| DR | Pfam: PF00001; 7tm_1; 1. | | | |
| DR | PRINTS: PRO1557; CHEMOKINER10. | | | |
| DR | PRINTS: PRO1558; CHEMOKINER11. | | | |
| DR | PRINTS: PRO1559; DUFFYANTIGEN. | | | |
| DR | PROSITE: PS00237; G_PROTEIN_RECPT_FL1; UNKNOWN_1. | | | |
| DR | PROSITE: PS00262; G_PROTEIN_RECPT_FL2; 1. | | | |
| KW | RECEPTOR. | | | |
| SQ | SEQUENCE 350 AA: 39530 MW; C5F7D9DC949CECCF CRC64; | | | |

Query Match 87.7%; Score 1596; DB 11; Length 350;

Best local Similarity 85.4%; Pred. No. 4e-137;

Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

| | | |
|----|----|---|
| QY | 1 | MALEONQSTDDYEEENEMNGTYDYSEYELICKEDYREFAKFLPYLTVIVIGLAGNS 60 |
| DB | 1 | MALEONQSTDDYEEENEMNGTYDYSEYELICKEDYREFAKFLPYLTVIVIGLAGNS 60 |
| QY | 61 | MVAIAIAYKKKTKTDYIINLAVADLLFLTPRWAVNAVHGWLGKIMCKITSALYT 120 |

```

Db 61 VVAIVAYKKQRTKTDVYIINLAVALDLLITLPMVAVNAVHGMILGKMKCKVTSALYT 120
      :|||||
Qy 121 LNFVSGMOFLACISIDRYVAATKVPVSGVGRKPCMIICFCVMAAILLSIPOLVEFYVND 180
      :|||||
Db 121 VNFVSGMOFLACISIDRYVAATKVPVSGVGRKPCMIICFCVMAAILLSIPOLVEFYVND 180
      :|||||
Qy 181 NARCIPIFPRLTGTSMKALIQMLEICIGFVVPFLIMGVCFYITARTLTKMPNIIKISRPLK 240
      :|||||
Db 181 NARCIPIFPRLTGTSMKALIQMLEICIGFVVPFLIMGVCFYITARTLTKMPNIIKISRPLR 240
      :|||||
Qy 241 VLLVAVVEFYITQLPYNVVFKCAIDIIYLSITSCNMSKRMDAIQVTESTALFHSCLNP 300
      :|||||
Db 241 VLLVAVVEFYITQLPYNVVFKCAIDIIYLSITSCNMSKRMDAIQVTESTALFHSCLNP 300
      :|||||
Qy 301 ILVYFMGASFKNYIMKVAKKYGSRROROSVEEPFDSGTEPTSTFSFI 350
      :|||||
Db 301 ILVYFMGASFKNYIMKVAKKYGSRROROSVEEPFDSGTEPTSTFSFI 350
      :|||||

```

RESULT 2

```

Q08QW9 PRELIMINARY; PRT; 350 AA.
ID 08QW9
AC 08QW9
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Chemokine receptor CCX CKR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA "Townson J.R., Nibbs R.J.: CCX CKR, a receptor for the lymphocyte-
RT attracting chemokines TECK (CCL25), SLC (CCL21) and MIP-3beta (CCL19):
RT comparison to human CCX CKR."
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY072796; AAL68400.1; -.
DR EMBL: AY072938; AAL68962.1; -.
KW Receptor.
SQ SEQUENCE 350 AA; 39544 MW; D017CC29749CECD5 CRC64;

```

Query Match 87.6%; Score 1593; DB 11; Length 350;
 Best local similarity 85.1%; Pred. No. 7.5e-137;
 Matches 298; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

```

Qy 1 MALEONOSTDYIEENENGTYYDSQYELICIKEDVREFAKVELLPLTVFYIQLAGNS 60
      :|||||
Db 1 MALELNOSAEYEEENENYHDYSQYEVICIKEDVROFAKVELLPLTVFAFYIQLAGNS 60
      :|||||
Qy 61 MVVAIVAYKKQRTKTDVYIINLAVALDLLITLPMVAVNAVHGMILGKMKCKVTSALYT 120
      :|||||
Db 61 VVAIVAYKKQRTKTDVYIINLAVALDLLITLPMVAVNAVHGMILGKMKCKVTSALYT 120
      :|||||
Qy 121 LNFVSGMOFLACISIDRYVAATKVPVSGVGRKPCMIICFCVMAAILLSIPOLVEFYVND 180
      :|||||
Db 121 VNFVSGMOFLACISIDRYVAATKVPVSGVGRKPCMIICFCVMAAILLSIPOLVEFYVND 180
      :|||||
Qy 181 NARCIPIFPRLTGTSMKALIQMLEICIGFVVPFLIMGVCFYITARTLTKMPNIIKISRPLK 240
      :|||||
Db 181 NARCIPIFPRLTGTSMKALIQMLEICIGFVVPFLIMGVCFYITARTLTKMPNIIKISRPLR 240
      :|||||
Qy 241 VLLVAVVEFYITQLPYNVVFKCAIDIIYLSITSCNMSKRMDAIQVTESTALFHSCLNP 300
      :|||||
Db 241 VLLVAVVEFYITQLPYNVVFKCAIDIIYLSITSCNMSKRMDAIQVTESTALFHSCLNP 300
      :|||||
Qy 301 ILVYFMGASFKNYIMKVAKKYGSRROROSVEEPFDSGTEPTSTFSFI 350
      :|||||
Db 301 ILVYFMGASFKNYIMKVAKKYGSRROROSVEEPFDSGTEPTSTFSFI 350
      :|||||

```

RESULT 3

```

Q09ESK1 PRELIMINARY; PRT; 221 AA.
ID 09ESK1
AC 09ESK1
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Putative G-protein coupled receptor GPCR4 (Fragment).
GN GPCR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARLAN SPRAGUE-DAWLEY;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.:
RT "Identification and characterization of novel G-protein coupled
RT receptors expressed in regenerating peripheral nerve."
RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF090348; AAG24470.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1557; CHEMOKINER10.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 221 221
SQ SEQUENCE 221 AA; 24342 MW; 5622DD607378A6C CRC64;

```

Query Match 50.1%; Score 912; DB 11; Length 221;
 Best local similarity 83.3%; Pred. No. 4e-75;
 Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

```

Qy 96 FMAVNAVHGMVLGKIMCKITSLALYLVNFVSGMOFLACISIDRYVAATKVPVSGVGRKPCW 155
      :|||||
Db 19 FMAVNAVHGMILGKIMCKITSLALYLVNFVSGMOFLACISIDRYVAATKVPVSGVGRKPCW 78
      :|||||
Qy 156 IICFCVMAAILLSIPOLVEFYVNDNARCIPIFPRLTGTSMKALIQMLEICIGFVVPFLI 215
      :|||||
Db 79 IICFCVMAAILLSIPOLVEFYVNDNARCIPIFPRLTGTSMKALIQMLEICIGFVVPFLI 138
      :|||||
Qy 216 MGVCYITARTLTKMPNIIKISRPLKVLTVVYVFTVQLPYNVVFKCAIDIIYLSITSC 275
      :|||||
Db 139 MGVCYITARTLTKMPNIIKISRPLKVLTVVYVFTVQLPYNVVFKCAIDIIYLSITSC 198
      :|||||
Qy 276 NMSKRMDAIQVTESTALFHSCL 298
      :|||||
Db 199 NMSKRMDAIQVTESTALFHSCL 221
      :|||||

```

RESULT 4

```

Q09Q006 PRELIMINARY; PRT; 369 AA.
ID 09Q006
AC 09Q006
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chemokine receptor CCR9 (CC chemokine receptor 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9248139; PubMed=10229797;
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RT receptor for the chemokine TECK."

```


Db 17 YVDSSEFTTVEGDDVDNFMCDKSAVRAFRGQYEPPLVYVILGGLNLTVMVYIHLFR 76

Qy 71 KO-RRTDYVYIINLAVADLLFTLPFAVNAVHGVGLKIMCKITSAIYLTNEVSGMOF 129

Db 77 QRLKMTDITLYINLAVADDFLGLTLPFAVNAVHGVGLKIMCKITSAIYLTNEVSGMOF 136

Qy 130 LACISIDRYVAVTKVPSOSGVK-P-----CWITCFVMAAILLSIPOLVFYVND--NA 182

Db 137 LVCISVDRVAVTVQTTMAONSKRQLSCSKFVCAVWVLAVLLAPFEMFANVKELDGOF 196

Qy 183 RCIPFPRYLGTSKRALIOMLEICIGFVVPFLIMGVCFITARTLTKMPNKRISPLKVL 242

Db 197 YCTVYVWSNQRRTKIVLVGLDIOGFCPLPILVAFYFCAGIIRTLTKRSQKHAKLAVI 256

Qy 243 LTVVVFVITQLPYINVKFCRAIDIIYSLTSCNMSKRMIDIAOVTSIALFHSCLNPL 302

Db 257 LVVAVVFLVSLQLPYNSVYVMEATQANSTQDCSAKRFNVVSOVLKSLAVTHACLNPL 316

Qy 303 YVFMGASFKNVYVAKKYGSM 324

Db 317 YVFGVFRFRDILKLRITVHGM 338

RESULT 7

Q9N020 PRELIMINARY; PRT: 343 AA.

AC 09N020: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE STRL33.

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cebidae; Cercopithecinae; Cercopithecus.

NCBI_TaxID=9531.

OX NCBI_TaxID=9531.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20261727; Pubmed=10799581;

RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W., Kirchhoff F.,

RT "Simian immunodeficiency virus utilizes human and sooty mangabey but not rhesus macaque STRL33 for efficient entry."

RL J. Virol. 74:5075-5082(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W., Kirchhoff F.,

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF237559; AAF68392.1;

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCR_Rhodopsn.

DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.

SQ SEQUENCE 343 AA; 39589 MW; A75B7A0751C1455 CRC64;

Query Match 31.8%; Score 578; DB 6; Length 343;

Best Local Similarity 33.7%; Pred. No. 1.5e-44;

Matches 120; Conservative 73; Mismatches 131; Indels 32; Gaps 8;

Qy 10 DYVEENENMGTYDYQYELICIKEDVREFAKVFLPVFLTYVIGLAGNSMVAIYAY 69

Db 5 DVEDEDEFNSFNDSQKE-----HDFLOFSKVLPCMLVVFVCGVNSLVYISITY 60

Qy 70 KKRRTDYVYIINLAVADLLFTLPFAVNAVHGVGLKIMCKITSAIYLTNEVSGMOF 129

Db 61 HKQSLTDLVFLNPLADLVFVCTLPFAVNAVHGVGLKIMCKITSAIYLTNEVSGMOF 120

Qy 130 LACISIDRYVAVTKVPSOSGVKPCW--IICFCVMAAILLSIPOLVFYVND--NDNR 183

Db 121 LNCITVDRIVVYKATKAVNQAKRMTGKIVICLLIWTISLVSLPQIITGNVFLDKLI 180

Qy 184 CIPFPRYLGTSKRALIOMLEICIGFVVPFLIMGVCFITARTLTKMPNKRISPLKVL 243

Db 181 C-----HYHDEISTVLAQMTLGFLLPLTMTVCVSVIKRLIHLAGGOKRIRSIIF 235

Qy 244 TVVVFVITQLPYINVKFCRAIDIIYSLTSCNMSKRMIDIAOVTSIALFHSCLNPL 303

Db 236 LVVAVVFLVSLQLPYNSVYVMEATQANSTQDCSAKRFNVVSOVLKSLAVTHACLNPL 316

Qy 304 VFMGASFKNVYVAKKYG-----SWRORQSVEEPPDESEPTPTSTFSI 350

Db 290 AFVSLFRKNVYVAKKYG-----SWRORQSVEEPPDESEPTPTSTFSI 350

RESULT 8

Q9EO16 PRELIMINARY; PRT: 351 AA.

AC 09EO16: 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Chemokine receptor CXCR6.

GN CXCR6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6.

RX MEDLINE=21177382; Pubmed=11017100;

RA Matloubian M., David A., Engel S., Ryan J.E., Cyster J.G.,

RT "A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo."

RL Nat. Immunol. 1:298-304(2000).

DR EMBL: AF301018; AAG34367.1;

DR MGD: MGI:1934582; CXCR6.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCR_Rhodopsn.

DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SQ SEQUENCE 351 AA; 40468 MW; 5658788372B4C65A CRC64;

Query Match 31.1%; Score 566.5; DB 11; Length 351;

Best Local Similarity 35.4%; Pred. No. 1.7e-43;

Matches 127; Conservative 70; Mismatches 125; Indels 37; Gaps 10;

Qy 10 DYVEEN--ENMGTYDYQYELICIKEDV--EFAKVFPLPVFLTYVIGLAGNSMVAI 65

Db 12 DGHYGDWFLFNSSDNSQ-----ENKRLKREKVFPLPVYLVVFVFGGLGNSVLII 64

Qy 66 YAYYKORTKTDVYIINLAVADLLFTLPFAVNAVHGVGLKIMCKITSAIYLTNEV 125

Db 65 YIFVYKLTLDVFLNPLADLVFVCTLPFAVNAVHGVGLKIMCKITSAIYLTNEV 124

Qy 126 GQWFLACISIDRYVAV--TVPSOSGVKPCW--IICFCVMAAILLSIPOLVFYVND 180

Db 125 SMLTLCITVDRFVYVQATKAFNRQAKM--IMQVVICLLIWTISLVSLPQIITGNV 183

Qy 181 NARCIPIPRYLGTSKRALIOMLEICIGFVVPFLIMGVCFITARTLTKMPNKRISPL 240

Db 184 IDKLT--CQYHSEISTVLAQMTLGFLLPLTMTVCVSVIKRLIHLAGGOKRIRSL 240

Qy 241 VLVVVFVITQLPYINVKFCRAIDIIYSLTSCNMSKRMIDIAOVTSIALFHSCLNPL 300

Db 241 IIFLVAVVFLVSLQLPYNSVYVMEATQANSTQDCSAKRFNVVSOVLKSLAVTHACLNPL 294

Qy 301 ILVFMGASFKNVYVAKKYG-----SWRORQSVEEPPDESEPTPTSTFSI 350

Db 295 VLVAVVGLKFRKNVYVAKKYG-----SWRORQSVEEPPDESEPTPTSTFSI 351

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RESULT 9
09BDS6 PRELIMINARY; PRT; 343 AA.
ID 09BDS6
AC 09BDS6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Orphan seven transmembrane receptor STRL33.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX Wade-Evans A.M., Russell J., Jenkins A., Javan C.;
RT "Cloning and sequencing of cynomolgus macaque ccr3, gp15, and strl33:
RT potential coreceptors for HIV type 1, HIV type 2, and SIV.";
RL AIDS Res. Hum. Retroviruses 17:371-375(2001).
DR EMBL: AF291671; AAK25742.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor; Transmembrane
SQ SEQUENCE 343 AA; 39472 MW; 0961328948E7784 CRC64;

Query Match 31.1%; Score 566; DB 6; Length 343;
Best Local Similarity 33.1%; Pred. No. 1.8e-43;
Matches 118; Conservative 73; Mismatches 133; Indels 32; Gaps 8;

QY 10 DYYEENEMNGTYDSQYELICIKEDVR--EFAKVFPLVFLTYFVIGLAGNSVVAI 69
DB 5 DHYEDGDFLNFNSDSQSE---HODFLOFRKVFPCMYLVFVCGLAGNSLVLVISIFY 60
QY 70 KQRTKTDVYIILNLAVALDLFTLPFMAVNAVHGVNLGKIMCKITSALTYLNFVSQMF 129
DB 61 HKLQSLTDVFLNPLADLVFVCTLPFMTYAGIHHEMIGQWCKTLGVTYINFTSLMI 120
QY 130 IACISIDRYAVATKVP--QSGVGKPCW--IICFCVMAAILSTIPOLVFTV--NDNAR 183
DB 121 LITCITDRIYVVKATKAYNOQAKRMGTGKVCILIVIVISLVSPLQIYGNVFLDKLI 180
QY 184 CIPRPRVLGTSMAKLIOMLEICIGFVVPFLMGVCYFITARLTKMKMNKISRPKVL 243
DB 181 C-----GHDEEISTVVLATQTFGLFPLAMIVCYSVIITKTLHAGGFQKHSKLTIF 235
QY 244 TVIVFIVTQLPYNIIVKFCRAIDILYSLTSCNMSKRMIDIAIOVTESIALFHSCLNPLY 303
DB 236 LYMAVFLITQTFPNLVKLIRSTRMEYAMTSFHYT-----IIVETALAYLRACINPLY 289
QY 304 VEMGASFKNYVMAKAYG-----SWRRQSVSEEPFDSGTEPTSTFSI 350
DB 290 AVFSIKFRKFNKLVKIDIGCLPYLGVSQWKSSEDNSK--TFSASHNVEATSMFQL 343

RESULT 10
Q9ERH5 PRELIMINARY; PRT; 351 AA.
ID Q9ERH5
AC Q9ERH5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative chemokine receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-C57BL/6; TISSUE=SPLEEN;
RA Sato H., Taniguchi M.;
RT "Molecular cloning of a putative chemokine receptor preferentially
RT expressed in mouse lymphocytes.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF305709; AAG31284.1; -
DR MGI: 1934582; Cxcr6.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 40511 MW; B00E3134D2B4DIED CRC64;

Query Match 30.9%; Score 561.5; DB 11; Length 351;
Best Local Similarity 35.4%; Pred. No. 4.7e-43;
Matches 127; Conservative 69; Mismatches 126; Indels 37; Gaps 10;

QY 10 DYYEEN--EMNGTYDSQYELICIKEDVR--EFAKVFPLVFLTYFVIGLAGNSVVAI 65
DB 12 DGHYEGDFLNFNSDSQSE---ENKRFLEKFEVFLPCVYLVFVFGLAGNSLVLI 64
QY 66 YAYKKQRTKTDVYIILNLAVALDLFTLPFMAVNAVHGVNLGKIMCKITSALTYLNFVS 125
DB 65 YIFQKRTLDVFLNPLADLVFVCTLPFMAVNAVHGVNLGKIMCKITSALTYLNFVS 124
QY 126 GMPFLACISIDRYAV--TRVPSQSGVGPW--IICFCVMAAILSTIPOLVFTVND 180
DB 125 SMLTITCITDRIYVVKATKAYNOQAKRMGTGKVCILIVIVISLVSPLQIYGNVFL 183
QY 181 NARCIPIPRVLGTSMAKLIOMLEICIGFVVPFLMGVCYFITARLTKMKMNKISRPK 240
DB 184 IDKLI---COYHSEISTVVLATQTFGLFPLAMIVCYSVIITKTLHAGGFQKHSKLT 240
QY 241 VLLTVIVTQLPYNIIVKFCRAIDILYSLTSCNMSKRMIDIAIOVTESIALFHSCLNPLY 300
DB 241 IIFLVAVFLITQTFPNLVKLIRSTRMEYAMTSFHYT-----FKYAIYVETALAYFRACLN 294
QY 301 ILVVMGASFKNYVMAKAYG-----SWRRQSVSEEPFDSGTEPTSTFSI 350
DB 295 VLVAVFLGKFRKFNKLVKIDIGCLSHLVSSQWKSSEDNSK--TCSASHNVEATSMFQL 351

RESULT 11
Q9HCAS PRELIMINARY; PRT; 342 AA.
ID Q9HCAS
AC Q9HCAS;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Mutant G protein-coupled receptor STRL33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97311099; PubMed=9166430;
RA Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-
RT 1.";
RL J. Exp. Med. 185:2015-2023(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA An P., Winkler C., O'Brien S.J.;
RT "The influence of a STRL33 mutant on the course of HIV-1 infection.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

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QY 182 A---RCIPFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLKM-MPNKISR 237
 DB 183 GTRAMCDBRVYSESGNIMMTFRQHLFVGLVLPGLVILCYCLITIKLSQSGKGLQKR 242
 QY 238 PLKVLVTVIVFVITQLPYNIKFCRAIDIIYSILITSCNMSKRMDAIOVETISALFHC 297
 DB 243 ALKFTTIIILIAFFICMLPVCIALIVDLVILNLYQVNCITQHNHETWIFETEGIAFYHC 302
 QY 298 LNPILYFMGASFKNYMKAKKGSWRROSVSEFPPEPTEPTSTFS 349
 DB 303 LNSTLYAFVGLYKFK---KSKAKSLIVNSKSSSLIKLISKKRGLSSVSTES 350

RESULT 14

Q91ZH4 PRELIMINARY; PRT; 360 AA.
 AC Q91ZH4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE C-C-chemokine receptor 4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRAIN-LEM;
 RA Garcia G.E., Chen S., Xia Y., Harrison J., Wilson C.B., Johnson R.J.,
 RA Bacon K.B., Feng L.;
 RT "Mononuclear cell-infiltrate inhibition by blocking macrophage-derived
 RT chemokine results in attenuation of developing crescentic
 RT glomerulonephritis."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF432872; AAL30398.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO1559; DUFFYANTIGEN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL2; 1.
 KW Receptor.
 SQ SEQUENCE 360 AA; 41218 MW; 50956CD299E1F8B CRC64;

Query Match 29.4%; Score 534.5; DB 11; Length 360;
 Best Local Similarity 34.7%; Pred. No. 1.4e-40;
 Matches 113; Conservative 67; Mismatches 127; Indels 19; Gaps 6;

QY 3 LEQNSQDYEEENMGTYDYSOYELICIKEDYREFAKVPFLVFLTVFVYGLAGNSMY 62
 DB 1 MNATEVVDITQDEETVNSYFDESILPKPCKEGKAFGEVFLPLVSLVFLGLFGNSVY 60
 QY 63 VAIAAYKKOKRTDYIINLAVALDLLFTLPRAVANAAGWLGKIMKITSALTIN 122
 DB 61 VLVEFKRKRLKSMQVYLLNLALISDLFLVSLPFGYAADQWVGLGKIIISMTLVG 120
 QY 123 FVSGMOFLACISIDRYAAVTV-----PSQSGVKPCWILCECVMAAILLSIPOLVF 175
 DB 121 FYSGLFELMMSIDRYLAIVAVSLAKRILTYGV-----ITSLITMSVAVFSLRDLF 175
 QY 176 YTV--NDNARCIPIFPYRLGTSMKALIQMLEI-CIGFVVPFLIMGVCYFTARTLKM 231
 DB 176 STCDTENNHCTKYQYS--VNSTWVKVLSLEINVLGLVIFPLGIMLFCYSMIIRTRHCK 233
 QY 232 NIKISRLKVLTVIVFVITQLPYNIKFCRAIDIIYSILITSCNMSKRMDAIOVETI 291
 DB 234 NEKNRAVRMLFAVAVVFLGFWTPYNAVFLLETL-VELEVLDQCTERYLDYALQATETL 292
 QY 292 ALFHSCLNPLIYFMGASFKNYMKV 317
 DB 293 AFHICLNPLIYFELGEKFRKIYALQ 318

RESULT 15
 Q8VHP3 PRELIMINARY; PRT; 361 AA.
 AC Q8VHP3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CC-chemokine receptor 4.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jopling L.A., Sabroe I., Andrew D.P., Mitchell T.J., Li Y.,
 RA Hodge M.R., Williams T.J., Pease J.E.;
 RT "The identification, characterization and distribution of guinea pig
 RT CCR4 and epitope mapping of a blocking antibody."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF431971; AAL57488.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL2; 1.
 KW Receptor.
 SQ SEQUENCE 361 AA; 41064 MW; 9304E897D4FD6839 CRC64;

Query Match 29.1%; Score 529; DB 11; Length 361;
 Best Local Similarity 36.0%; Pred. No. 4.4e-40;
 Matches 118; Conservative 66; Mismatches 104; Indels 40; Gaps 10;

QY 9 TDYEEENMGTYDYSOYELICIKEDYREFAKVPFLVFLTVFVYGLAGNSMYAIVAY 68
 DB 17 SNYVNESSVPG-----CTKGVAKAFGLFLPLYSVFLFGLGNSVVLVLEK 67
 QY 69 YKKOKRTDYIINLAVALDLLFTLPRAVANAAGWLGKIMKITSALTINLVYSGMQ 128
 DB 68 YKLRSMITDYIINLAVALDLLFTLPVSLPFGYAAADQWVGLGCKMISIVLVGFSGIF 127
 QY 129 FLACISIDRYAAVTV-----KVPSSQ-GVGKPCWILCECVMAAILLSIPOLVF--YTV 178
 DB 128 FIVLMISIDRYLAIVHGVESMRVNTFTYGV-----ITSLTAVAVFASLPGLFSTCYTE 182
 QY 179 NDNARCIPIFPYRLGTSMK-ALIQMLEI-CIGFVVPFLIMGVCYFTARTLKMPIKIS 236
 DB 183 RNHTSC--KTRSANSTWVKVLSLEINVLGLVIFPLGIMLFCYSMIIRTHCKSKKN 239
 QY 237 RPLKVLTVIVFVITQLPYNIKFCRAIDIIYSLI-----ISCNMSKRMDAIOVETI 291
 DB 240 KAVKMLFAVAVVFLGFWTPYNAVFLLETL-VELEVLDQCSLEKYLDPALQATETL 293
 QY 292 ALFHSCLNPLIYFMGASFKNYMKVAK 319
 DB 294 AFHICLNPLIYFELGEKFRKIYVLEK 321

Search completed: March 14, 2003, 16:13:21
 Job time : 37 secs

